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for 6q-linked retinopathies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. and Weber, B.H.F.
Assessment of a novel interphotoreceptor matrix gene (IPM150)
localized to 6q14.2-q15 in autosomal dominant stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI)
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Direct Submission
Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am
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746 'TGATAGTCAAAATGATCATAAGCCAGGTTTGCTTCCACCTTCCCTGAAAATTTTACTCAC 805
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1 (bases 1 to 816)
Felbor, U., Gthig,A., Sauer,C.G., Marquardt,A., Kohler,M., Schmid,M., and Weber,B.H.
Genomic organization and chromosomal localization of the
                                                                                                                                                                                                                                  3132 ttaaaagaaactgaggttcagatacacataccatggaaaaatcttactttcttgttact
                                                                                                                                                                                                                                                                                                    2832 àgatcatttgcaacaagcatagcttacttattgtttagggactgaacaatttattgggaa
                                                                                                                                                        806 AGATCATTTGCAACAAGCATAGCTTACTTATTGTTTAGGGACTGAACAATTTATTGGGAA
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/organism="Homo sapiens" /db_xref="taxon:9606"

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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 194704)
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/map="6q14.2-q15"
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/gene="IPM150"
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Best Local Similarity 99.6%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 435) NCI CGAP http://www.ncbl.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

AA815118 AA815118.1 GI:2884714

Homo sapiens

REFERENCE AUTHORS TITLE

JOURNAL

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human.

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

Tunor Gene Index Uppublished (1997)
On Jan 17, 1998 this sequence version replaced g1:2045394.
Contact: Robert Strausberg, Ph.D.
Talsue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
CONA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

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9b_9ss14:*
9b_9ss15:*
9b_9ss16:*
9b_9ss17:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1		عد (
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	22		n	33	7398	2 oq03g11.

CONA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1672 Std Error: 0.00
Seq primer: -40ml3 fwd.ET from Amersham
High quality sequence stop: 381.

source

FEATURES

3213 ggtgatgaagccaaccettgcaagtttcaggcetgtaatgaattttcagagtgtetggte 3272 435 GGTGATGAAGCCAACCCTTGCAAGTTTCAGGCCTGTAATGAATTTTCAGAGTGTCTGGTC 376 5.1%; Score 214; DB 31; Length 435; 100.0%; Pred. No. 1.2e-102; 11ve 0; Mismatches 0; Indels Query Match
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0; Gaps

constructed by Bento Soares and M. Fatima Bonaldo. 109 c 74 g 125 t

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BASE COUNT ORIGIN

ALIGNMENTS

AA815118 435 bp mRNA EST ' 05-WAR-1998 oa88h10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1319395 similar to TR:P70628 P70628 PG10.2. ;, mRNA sequence.

RESULT 1
AA815118/c
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33278
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334049: contig of 771 bp in length
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34049 34148: gap of
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34034: gap of
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35703: contig of 786 bp in length
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35658: contig of 759 bp in length
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37545: contig of 765 bp in length
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57: gap of 100 bp
18237: contig of 780 bp in length
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44649: gap of 100 bp
44647: contig of 778 bp in length
45527: gap of 100 bp
46321: contig of 794 bp in length
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Rattus norvegicus Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 4368) Wang,X., Brownstein,M.J. and Young,W.S. 3rd. Sequence analysis of F010.2, a gene expressed in the pineal gland and the outer nuclear layer of the retina Brain Res. Mol. Brain Res. 41 (1-2), 269-278 (1996) 22966 GGATAATACCTITCAAGCTGCATGGCCCTCAGCAGATGAATCCATCACCAGCAGTATTCC 22907 ggataatacettteaagetgeatggeecteageagatgaatecateaeeageagtattee 1489 Wang, X., Brownstein, M.J. and Young, W.S.
Direct Submission
Submitted (30-oct-1966) LCMR, NIMH, 36 Convent Drive, MSC 4068, Bethesda, MD 20892-4068, USA 13-NOV-1996 ö Length 77043; 46322 46421: gap of 100 bp 47202 47201: contig of 780 bp in length 47302 47301: contig of 780 bp in length 48095 gap of 100 bp 48195 gap of 100 bp 48195 gap of 100 bp 49827 gap of 100 bp 49827 gap of 100 bp 49827 gap of 100 bp 5926 gap of 100 bp 6926 gap of 10 0; Indels RNU76717 4368 bp mRNA ROLL Rattus norvegicus PG10.2 mRNA, complete cds. U76717 Query Match 3.0%; Score 125; DB 71; Best Local Similarity 100.0%; Pred. No. 1.9e-60; Matches 125; Conservative 0; Mismatches 0; U76717.1 GI:1667596 (bases 1 to 4368) 22846 TCCTT 22842 1550 tcctt 1554 97038366 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM 1430 REFERENCE AUTHORS TITLE MEDLINE REFERENCE AUTHORS TITLE JOURNAL RESULT RNU76717 JOURNAL 요 g 요 à 8

kielin,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
Levine,R., Lieu,C., Liu,G., Looke,K., Macdonald,P., Marquis,N.,
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Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigillo,J.,
Vassillev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Direct Submission

Submitted (25-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE JOURNAL

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research

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/ LEADS 14 LO. - *MELDER ISLATILF LIGGRILVS Y SEET OD RAHAVAVLS PKES
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SLSSVENAMKYNPAYESRLAGCEQYEKPYSQHPFYSSASEEVIGGLSREEIRQMYESS
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2 (bases I to 65674)

Birran, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Buskett, G., Bodusjalter, B. Brown, A., Burkett, G., Canpoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galaqan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grand, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 65674)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 21, clone RP11-65K18 DNA HTG 25-MAR-2000 21 clone RP11-65K18 map 21, LOW-PASS Indels ch 0.9%; Score 38; DB 12; L
1 Similarity 100.0%; Pred. No. 7.7e-10;
38; Conservative 0; Mismatches 0; Homo saptens chromosome 21 SEQUENCE SAMPLING. AC026980.1 GI:7328857 HTG; HTGS_PHASE0. Homo sapiens AUTHORS TITLE JOURNAL REFERENCE AUTHORS REFERENCE

* NOTE: This record contains 84 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will 65 764: 984 Contig of 692 bp in length 1457 1556: 9ap of 100 bp 1557 2235: contig of 692 bp in length 1558: 9ap of 100 bp 1557 2235 2335: contig of 679 bp in length 2236 2335: gap of 100 bp 2336 3302: contig of 667 bp in length 303 3102: 9ap of 100 bp 3103: 9ap of 100 bp 3789: contig of 687 bp in length 3790 3889: gap of 100 bp 4694 653: contig of 685 bp in length 6594 653: contig of 685 bp in length 6594 657: contig of 689 bp in length 6588 657: contig of 689 bp in length 6588 657: gap of 100 bp 658 6942: contig of 659 bp in length 658 6542: contig of 659 bp in length 658 7711: contig of 659 bp in length 7712 7811: gap of 100 bp 7712 7811: gap of 100 bp 7712 7811: gap of 100 bp 70 10169: gap of 100 bp 10 length 106 10845: contig of 676 bp in length 16 10845: gap of 100 bp 100 bp 10 length 13 11732: gap of 100 bp 100 b 100 bp f 697 bp in length 664: contig of 664 bp in length 100 bp f 684 bp in length contig of contig of 2 7811: gap of 8 8488: cont 9 8588: gap of 9 9285: cont 9385: gap of 10069: cor be preserved. 8489 8589 9286 9386 10070 10170 10846 10946 11633

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9b_9ss15:*
9b_9ss16:*
9b_9ss17:*
9b_9ss18:*
em_9ss13:*
gb_gss13:*
1117 ... 120 ... 1221 ... 1222 ... 1233 ... 124 ...
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ripti	H38604 yp	78 AA296278 EST10	Н38594 у	163 AA326863)80 AQ234080	.51 AI632451	182 AI695882	183 AI093483	.61 AW303461	114 AQ87111	37 AW263637	.04 AQZ84104	46 AV267846	T53905 yb83£06	.77 AI266177 gg87b	252 AQ842252 T136	05 AA550505 1662m	-M-IO 801843103 01-M-	415	954 AO404954 HS 5	129 AQ412129 RPCI	185 AA522085 vil6f0	50 AW633450 bl07h0	239 AQ842239 T1361	37 AW687237	W29432 mb99e0	39 AI947789 6030;	33 AW486083	LS AV243915 AV24	50 AV350030	Z17817 HSDHEOO3	R58213 G	72 AV122672 AV1226	82 AQ276082	95 AV264595 AV2645	68 AQ080468	891 1(2)k0	46/ AD4 AD4 / / 46
日	H386(AA296	H3855	AA326	AQ234	AI632	AI695	AI093	AW303	A087	AW263	AUZBA	AV267	T5390	AI266	5 AQ84	AA550	AING	9 AZ05	2 A040	2 AQ41	AA522	AW633	5. A084	AW687	W2943	AI947	AW486	AV243	AV350	21781	R5821	AV122	AQ276	AV264	AQ080	A0025	804/
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ALIGNMENTS

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H38604 405 bp mRNA EST 16-AUG-1995 yp48e04.rl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190686 5', mRNA sequence. RESULT 1 H38604 LOCUS DEFINITION

The Washu-Werck EST Project
Unpublished (1995)
On May 18, 1998 this sequence version replaced gi:3138652.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 234
High quality sequence stops: 289
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
Insert Length: 2534
Seq primer: Mi3RPI Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

(bases 1 to 405)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohling,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and 1262 gaaattgetggateaetgeeageetttggteetgaeaeceaateagagetgeeeaatet 1321 1382 cttgagacagtggacggagcagagcatggtctacctgacacttcttggtctccacctgct 1441 ő Query Match 9.6%; Score 312; DB 85; Length 405; Best Local Similarity 100.0%; Pred. No. 2.9e-157; Matches 312; Conservative 0; Mismatches 0; Indels /clone_lib-"Soares retina N2b4HR" /sex-"male" 1. 405 /organism="Homo sapiens" /db_xref="EGD8:3847095" /db_xref="taxon:9606" /clone="iMAGE:190686" High quality sequence stop: 289. Location/Qualifiers GI:908103 Homo sapiens H38604 H38604.1 ACCESSION VERSION KEYWORDS SOURCE ORGANISM BASE COUNT ORIGIN REFERENCE AUTHORS FEATURES ö ద ò 셤 გ ò

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/organism="Homo sapiens"
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AA296278
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AUTHORS
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/dev_stage="adul
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 561)
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W26960 561 bp mRNA EST 08-MAY-1996
16h10 Human retina cDNA randomly primed sublibrary Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macke, J., Smallwood, P. and Nathans, J.
Adult Human Retina cDNA
Dupublished (1996)
On May 10, 1995 this sequence version replaced g1:805808.
Dr. Jeremy Nathans
Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
JOHNS HOPKINS School of Medicine
T25 North Wolfe Street, Baltimore, MD 21205
Fax: 410 614 0827
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99.3%; Pred. No. 2.4e-132;
iive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: CITITGAGCAAGITCAGCCTGGITAAGI
BACKWARD: GAGGIGGCITATGAGIATITCTTCCAGGGIAA
Seg primer: GGGIAAAAAGCAAAAGAAIT.
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W26960.1 GI:1306188
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

I (bases 1 to 298)

Bult.c.J., Lee, N. H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

Rilt.c.J., Lee, N. H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J. Fine, L.D.,

Glodek, A., Gnebm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,

Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shriey, R.,

Bednarik, D.P., Fergy, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Dinke, D., Fengy, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

Kozak, D.L., Kunsch, C., Hung, J., Xu, C., Hastings, G.A.,

Kozak, D.L., Weily, F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Kozak, D.L., Wang, W.M., R. Rosen, C.A., Hastings, G.A.,

Kaymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Kaymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Kaymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Kaymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Kaymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Kaymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Kaymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Kaymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Kaymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Kaymond, J., Weille, J.C., Ruber, J.C.

Initial assessment of human gene diversity and expression patterns

AL Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA296278 298 bp mRNA EST 18-APR-1997
SZI10795 Umbilical vein endothelial cells II Homo sapiens conn 5'
AA296278
                                                                                          1406 catggtctacctgacacttcttggtctccacctgctatggcctctacctccctgtcagaa 1465
                                                                                                                                                                                                                                                                                                                                      For clone availability, additional sequence and expression information related to this EST, please check the TiGR Human Gene Seq primer: Mi3 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlavetigr.org
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The Institute for Genomic Research
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Length 405;

DB 85;

10.9%;

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( (Dases 1 to 405)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Rultann, M., Rucaba, T., Lehm, Lennon, G., Marra, M.,
Parsons, J., Riffain, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
Insert Size: 2534
High quality sequence stops: 289
Source: IMAGE Consortium, Lini
This clone is available royalty-free through Lini
ThAGE Consortium (info@image.lini.gov) for further information.
Seq primer: Mi3RPl
High quality sequence stop: 289.
High quality sequence stop: 289.
                                                   H38604 405 bp mRNA EST 16-AUG-1995
yp46804.rl Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:190686 5', mRNA sequence.
H38604 GI:908103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Washu-Merck EST Project
Onpublished (1995)
On May 19, 1998 this sequence version replaced g1:3138652.
Contact: Wilson Rk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                   1. .405
/organism="Homo sapiens"
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/sex="male"
    5 09:04:02 2000
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95

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Eukaryotta, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (basea 1 to 322)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Cline, T.R., Cotton, M.D., Earle-Hughes, J.F., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghaqen, N.S., Relley, J.M., Kelley, M.M., Fritchman, J.L., Geoghaqen, N.S., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palaques, R.F., McDonald, L.A., Nquyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Fergy, D.-F., Ferley, M.A., Coleman, T.A., Collins, E.J., Merwich, D.M., Kopi, D.-F., Ferley, R., Fischer, C., Hastings, G.A., Royamond, L., Wei, Y.F., Wing, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Li, H., Meissner, P.S., Olsen, R., Praser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                                                                                            1322 tttgctgttataacagaggatgctactttgagtccagaacttcctcctgttgaacccag 1381
                                                                                                                                                                                                                                                                                                                                                atggeetetacetecetgteagaageteeacetttetttatggeateaageatettetet 1501
                                                                                    1262 gaaattgctggatcactgccagcctttggtcctgacacccaatcagagctgcccacatt 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA326863 322 bp mRNA EST 20-APR-1997
EST30113 Cerebellum II Homo sapiens CDNA 5' end, mRNA sequence.
AA326863 GI:1979130
                                                                                                                                                                                             9
                                                                                                             12140200
On Jan 14, 1998 this sequence version replaced gi:1878018.
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                                            Indels
Score 354.4; DB 85;
Pred. No. 2.3e-81;
0; Mismatches 2;
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The Institute for Genomic Research
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Query Match 10.9
Best Local Similarity 99.0
Matches 377; Conservative
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Homo sapiens
                                                                  human.
                                             VERSION KEYWORDS SOURCE ORGANISM
AA721009/c/
                 DEFINITION
                                     ACCESSION
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22-JAN-1998 IMAGE:1269436 NA721009 435 bp mRNA EST 72.

NK89e03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAK
Similar to TR:P70628 P70628 PG10.2. ;, mRNA sequence
AA721009

AA721009.1 GI:2737144

REFERENCE AUTHORS TITLE NAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 435)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP), On Jan 19, 1998 this sequence version replaced gi:2151557.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Email: Robert_Strausbergenih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Sequencing Center information can be Bonaldo, Ph.D. cDN Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Seq Clone distribution: NCI-CGAP clone distribution inffound through the 1.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1678 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 416.
Location/Qualifiers

source

FEATURES

/organism="Homo sapiens"
/db_xref="taxon:9606"
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constructed by Bento Soares and M. Fatima Bonaldo. 128 BASE COUNT

ORIGIN

Gaps ó 4.9%; Score 204; DB 30; Length 435; 100.0%; Pred. No. 2.6e-97; tive 0; Mismatches 0; Indels (Best Local Similarity 100.0 Matches 204; Conservative Query Match

3223 ccaaccettgcaagtttcaggcetgtaatgaattttcagagtgtetggtcaaccetgga 3282

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3283 giggagaagcaaagigcagaigciicciggaiaccigagigigaagaagaacggcccigic 3342 요 ö

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3343 agagtetetgtgacetacageetgacttetgettgaatgatggaaagtgtgacattatge 3402

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Tumor Gene Index

Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2045613.

On Jan 19, 1998 this sequence version replaced gi:2045613.

On Jan 19, 1998 this sequence version replaced gi:2045613.

Contact: Robert Strausbergenth, Bh.D.

Tel: (301) 496-1550

Email: Robert Strausbergenth, Gov.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Preparation: W.G. Gregorian Library Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.AG. E. Consortium/Library

Lought: Length: Library Preparation Margerial Library Sequence Stop: 378.

High quality sequence stop: 378.

Location/Qualifiers
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information can be
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                AA744481 435 bp mRNA EST 22-JAN-1998
ny25401.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1272769 3'
similar to TR:P70628 P70628 PG10.2. ;, mRNA sequence.
305 AGAGICICIGIGACCIACAGCCIGACTICIGCITGAAIGAIGGAAAGIGIGACAITAIGC 246
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                                                             AA744481
AA744481.1 GI:2783245
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Gaps ö Length 435; Indels 4.7%; Score 194; DB 30; 100.0%; Pred. No. 5.6e-92; tive 0; Mismatches 0; Matches 194; Conservative Best Local Similarity 127 Query Match BASE COUNT ORIGIN ò a

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September 3, 2000, 17:40:05 ; Search time 2736.15 Seconds
(without alignments)
6712.693 Million cell updates/sec
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4165
1 cgggywaytttgaaaggaca.....aaaaactacgttaaaaaaa 4165
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                               OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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119: gb_gss16:*
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121: gb_gss17:*
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124: em_gss13:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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DB ID		1 AA81511	0 AA72100	0 AA74448	0 AA73698	0 AA76	04 AQ5608	3 AI73955	8 AI34625	0 C15921	7 AI24803	1 AA11217	1 AA08	5 AA36544	2 AA87697	2 AA86035	4 AI03316	9 AA62962	8 AI38176	0 AA77421	9 T30212	9 T516	5 AI20248	4 AI83006	6 AI19	4 AW17312	9 T33508	6 AI93669	1 AA0961	3 AI69943	1 W48841	4 AW57566	8 AA5876	8 AI37243	1 AA77700	1 D524	1 AA84610	3 AA96124	0 AW3165	7 AI27592	8 AI35964	3 AI69852	8 AI37243	9 T30585	0 AA77283	33 AA973982
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ALIGNMENTS

AA815118 435 bp mRNA EST 05-MAR-1998 oa88h10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1319395 3 similar to TR:P70628 P70628 PG10.2. ;, mRNA sequence.

RESULT 1 AA815118/C LOCUS DEFINITION

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E I (bases 1 to 43 bits)./www.ncbl.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gl:2045394.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenth.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
CDMA Libbary Preparation: M. Bento Soares, Ph.D., M. Fatima CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
Gound through the I.M.A.G.E. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 381. ö 3273 aacccctggagtggagaagcaaagtgcagatgcttccctggatacctgagtgtggaagaa 3332 Gaps ö Query Match 5.1%; Score 214; DB 31; Length 435; Best Local Similarity 100.0%; Pred. No. 1.2e-102; Matches 214; Conservative 0; Mismatches 0; Indels /organism="Homo sapiens"
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305 AGAGTCTCTGTGACCTACAGCCTGACTTCTGCTTGAATGATGGAAAGTGTGACATTATGC 246
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Glound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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High quality sequence stop: 416.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 435)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                            Tumor Gene Index (UGAP)

Uppublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2151557.

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Ph.D., Gerald Marti, M.D.

Bonaldo, Ph.D.

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Instruct, Cancer remome Anatomy Figlet (Corr), on Jan 19, 1998 this sequence version replaced gi:2045613.

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On Jan 19, 1998 this sequence version replaced gi:2045613.

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Email: Robert Strausbergenih.gov
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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library A
AA744481 435 bp mRNA EST 22-JAN-1998
Ny25401.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1272769 3'
similar to TR:P70628 P70628 PG10.2.;, mRNA sequence.
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp//image/image.html
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Seq primar: -40m13 fwd. Er from Amersham
High quality sequence stop: 347.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA736980 383 bp mRNA EST 22-JAN-1998
nx89a04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269390 3',
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1 (Bases 1 to 383)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Thmor Gene Index Unpublished (1997)
                                                               Confect: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
3293 aaagtgcagatgcttccctggatacctgagtgtggaagaacggccctgtcagagtctctg 3352
               constructed by Bento Soares and M. Fatima Bonaldo." 96 c 64 g 111 t
                                                                                                                                                                                                                                                                                          mRNA sequence.
AA736980
AA736980.1 GI:2767255
                                                                                                                                     3413 ggccatttgtaggt 3426
                                                                                                                                                        235 GGCCATTIGTAGGT 222
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AA736980/c
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Gaps

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Query Match 3.9%; Score 162; DB 30; Length 383; Best Local Similarity 100.0%; Pred. No. 6.8e-75; Matches 162; Conservative 0; Mismatches 0; Indels (

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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                               AA766994 202 bp mRNA EST 08-FEB-1998 oa41c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1307520 3' shilar to TR:P70628 P70628 PG10.2. ; , mRNA sequence. AA766994 GI:2819575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@hih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
3265 gtctggtcaacccctggagtggagaagcaaagtgcagatgcttccctggatacctgagtg 3324
                                                                                                                                               323 TGGAAGAACGGCCCTGTCAGAGTCTCTGTGACCTACAGCCTGACTTCTGCTTGAATGATG 264
                                3325 tggaagaacggccctgtcagagtctctgtgacctacagcctgacttctgcttgaatgatg
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                                                                                                                                                                                                                            Insert Length: 1669 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ww-bio.llni.gov/bbrp/1mage/1mage.html
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ORIGIN
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AI739559 447 bp mRNA EST 21-DEC-1999 w135a06.x1 NCI_CGAP_CO16 Homo sapiens cDNA clone IMAGE:2392210 3' smilar to TR:P70628 P70628 PG10.2. ;, mRNA sequence. AI739559.1 GI:5101540
 3485 gcccgtgatcataggcatcactattgcctccgtggttggacttcttgtcatct 3537
                   224 GCCCGTGATCATAGGCATCACTATTGCCTCCGTGGTTGGACTTCTTGTCATCT 276
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                                                                                    RESULT 7
A1739559/c
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AI346256/c
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Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 534)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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High Throughput Sequencing Center
Ginversity of Washington
for the Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Jate: 2089 row: B column: 16
Seq primer: T7
Class: BAC ends
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/sex-"male"
                                                                                                                                      3296 gigoagaigoticociggalacotgagigigaagaacggocotgicagagictotgiga 3355
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                                                                     3236 giilcaggooigtaaigaaitilcagagigiotoiggicaacoooiggagiggagagaagoaaa 3295
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                                                                                       and
                                                                                                                                                                                                                                                                                                AQS60890 534 bp DNA GSS 29-MAY-1999 HS_2089_B2_A08_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2089 Col=16 Row=B, genomic AQS60890
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                                   Gaps
                                                                                                                                                          Gaps
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                                                                                                                                                                                                          Query Match 2.7%; Score 113; DB 104; Length 534; Best Local Similarity 100.0%; Pred. No. 1e-48; Matches 113; Conservative 0; Mismatches 0; Indels 0
Length 202;
                                   Indels
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/clone="plate=2089 Col-16 Row-B"
 Score 120; DB 30;
Pred. No. 1.8e-52;
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                                   0; Mismatches
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2.9%;
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                   Best_Local Similarity 99.4
Matches 170; Conservative
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human.
   Query Match
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1. .447
/organism="Mono sapiens"
/organism="Taxon:9606"
/db_xref="taxon:9606"
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/lab_host="Daylon
/clone = "Organ: colon, Vector: pr773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco Ri; Plasmid DNA from the normalized library Norl_CGAP_Col0 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified colNas from a pool of 5,000 clones made from the same library (cloner)s lo57416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
31 a 108 c 89 g 119 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Grag Lennon, Ph.D.

CDNA Library Arrayed by: Grag Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Content of Stribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/Darp/image/image.html

Insert Length: 1596 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 428.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Sass 1 to 447)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2151197.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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1.5%; Score 62; DB 43; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 62; Conservative 0; Mismatches 0; Indels
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ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalaia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 21)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

I Onpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2284999.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Emall: Robert_Strausbergeih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.lnln.gov) for further information.

Insert Length: 2289 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 195.

Location/Qualifiers

I . . 221
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Fujiwara et al. (1995)
Uppublished (1995)
On Jul 7, 1999 this sequence version replaced gi:5407660.
Contact: Tsutoun Fujiwara
Otsuka GEN Research Institute
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
df3-10, Asgasuno Rawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI248036 221 bp mRNA EST 01-DEC-1998 qh63f09.x1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone lMAGE:1849385 3', mRNA sequence.
AI248036
                                                                                                                                                                                                                                                                                                                                                                    /cramism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GEN-408F04"
/clone_llb="Clontech human aorta polyA+ mRNA (#6572)"
1 54 c 45 g 45 t 6 others
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/clone_11b="Soares_fetal_liver_spleen_INFLS_S1"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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100.0%; Pred. No. 3.7;
tive 0; Mismatches 0;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index

Unpublished (1997)

On Apr 7, 1998 this sequence version replaced g1:3035630.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenth.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Prayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOI-CAPP clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:

Seq primer: -400P from Gibco
High quality sequence stop: 328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-*Crgan: colon; Vector: pT7T3D-Pac (Pharmacla) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I -01190(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Scares and M. Patima Bonaldo. "
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Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 204)
Fujiwara;T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C15921 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-408F04 5', mRNA sequence.
C15921 GI:1570628
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 353)
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                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             AI346256 353 bp mRNA EST 30-DEC-1998 qp49f04.xl NCI_CGAP_CO8 Homo sapiens cDNA clone IMAGE:1926367 similar to contains element MER22 repetitive element ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
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                                                                                               sequence.
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AUTHORS REFERENCE

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Indels

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Pred. No. 3.8;

Mismatches

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Z3-DEC-1997 mRNA EST 23-DEC-1997 zm6403:11 Stratagene fibroblast (#937212) Homo sapiens cDNA clone AA084038
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 249)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Hillier,L., Lennon,G., Becker,M., Le,M.F., Chiapelli,B.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,R., Soares,M.B., Tan,F., Thierry-Meg,J.,
Travaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                       194 TATCCACCTTTTGGGGAAGCAG 173
                                                                                                                                                                                                                                                                                                                                              AA084038.1 GI:1626094
     100.08;
                                                                              tatccaccttttggggaagcag
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Matches 22; Conservative
       Best Local Similarity 100. Matches 22; Conservative
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/organism="Homo sapiens"
/db_xref="e081:3919964"
/db_xref="taxon:9606"
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/note="Vector: pBluescript SR-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. W138
cell line. Average insert size. 0.8 kb; Uni-ZAP XR Vector;
-5 adaptor sequence: 5 GAATTCGCAGAGA 3' -3' adaptor
sequence: 5 CTCGAGTTTTTTTTTTTTTTTTTT 3'"
(Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
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1 (bases 1 to 228)

Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., Dubque,T., Favello,A., Gish,W., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkln,L., Rohlling,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., and Marga,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: estewatson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should beept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
97044478
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Location/Qualifiers
                                                                                                                                                                                                                                                      Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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                                                                                                                                                                                               0.5%; Score 22; DB 37; Length 221; ilarity 100.0%; Pred. No. 3.8; Conservative 0; Mismatches 0; Indels
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1. .249
/organism="Homo sapiens"
/db_xref="Reps:3919964"
/db_xref="taxon:9606"
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/clone="IMAGE:530453"
/clone="Lib="Stratagene fibroblast (#937212)"
/lab_host="SOLR calls (kanamycin resistant)"
/lab_host="Solr calls (kanamycin
Email: estewatson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
Kept in mind should you use this clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 339 Std Error: 0.00 Seq primer: -28M13 rev2 from Amersham.

Location/Qualifiers
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iive 0; Mismatches
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Length 228;

21; B

0.5%; Score 22;

Query Match

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AA365447

REFERENCE

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Antiquia cancer institute, Cancer benome Anatomy Figjer (Corry), Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-1550
Email: Robert_Strausberg@ih.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-Cape clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image./image./hml
Seq primer: -40ml3 fwd. ET from Amersham.
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/lab_host="DH10B"
/note="Vector: pAWP10; mRNA made from metastatic prostate
lesion of the bone, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman,
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Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 271)

NCI-GGAP http://www.ncbi.nlm.nlh.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 266) NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 3.8;
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/clone_11b="NCI_CGAP_Pr12"
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/organism="Homo sapiens"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; 
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Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Information reliated to this EST, please check the TiGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
        AA365447 253 bp mRNA EST 21-APR-1997
EST76221 Pineal gland II Homo sapiens cDNA 5' end, mRNA sequence.
AA365447
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AA876973 GI:2986050
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/db_xref="ATC (inhost):170174"
/db_xref="ATC (inhost):170174"
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/clone_lib="Pineal gland II"
/dev_stage="adult"
/note="Organ: pineal body; Vector: pBluescript SK-;
/note="Corgan: pineal body; Vector:
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Contact: Kerlavage, AR
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ö Gaps ö Query Match 0.5%; Score 22; DB 32; Length 271; Best Local Similarity 100.0%; Pred. No. 3.8; Matches 22; Conservative 0; Mismatches 0; Indels

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Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.

H38604 H38604.1 GI:908103 EST.

human.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 405)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	H38604 yp48e04.rl	STI	H38594 yp48c06.rl	ST3011	AQ234080 HS_2057_A	A1695882 ts87b06.x	b15b03	v19d01	nbeb	AW263637 xn81b12.x	3 2	V267	34.	q87b	1	99	Į.	A2054415 RPCI-23-4	e/UIU4.r	A0412129 RPCI-11-1	116f06.r	107h02	T13617	AQ253330 HS_2046_B	02/004	2020	9850	V243	AV350030 AV350030	V131195	HE0034	78 Feta	AV122672 AV122672	/6082 CITBI-E	54595 AV264595	U468 CIT-HSP-	77777	*//*0/ CIIBI-E	AUU41U51 AUU41U51	*000*0 DF.43004
SUMMARIES	DB ID	85 H38604	4 AA296	5 H38594	4 AA32686	n c	3 AI69588	5 AI09348	0 AW30346	16 AQ8711	0 AW26363	6 AU28410	AV26784	9 T53905	. ~	16 AQ8422	8 AA55050	5 AI843103	19 AZ054	6 ALL9//45	02 A04121	7 AA522085	9 AW633450	16 AQ8422	6 AQ25333	9 AWO8/23	A AT94778	. m	9 AV24391	1 AV35003	0 AV13119	2 2178	8 R58213	0 AV12267	6 AQ2/608	9 AV26459	3 AQU8046	3 AQU2589	100000000000000000000000000000000000000	S AUU41	#000#W# 7
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The Washis Ferry Materiston, N., Williams Duly, F., Montaginal, F. and Wilson, R.

The Wash Wash G. 1993 his sequence version replaced gi:3138652.

On May 18, 1998 this sequence version replaced gi:3138652.

Contact: Wilson RK
Washington University School of Medicine
(Add Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Email: estewatson.wustl.edu

Insert Size: 2534

High quality sequence stops: 289

Source: INAGE Consortium, Linn.

This clone is available royalty-free through Linn; contact the INAGE Consortium (infodimage.linl.gov) for further information.

Insert Length: 2534 Std Error: 0.00

Seq primer: MisRel

Incation/Qualifiers

In 405

source

FEATURES

ALIGNMENTS

H38604 405 bp mRNA EST 16-AUG-1995 yp48e04.rl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190686 5', mRNA sequence.

LOCUS DEFINITION RESULT H38604

/sex="male" /tissue tvpe="retina"	/dev_stage="55 year old" /lab_host="DH10B (ampicillin resistant)"	<pre>/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st</pre>	<pre>strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTTTTTTTTT</pre>	double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into	the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). The retinas were obtained from a 55 year old	Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly	provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento	Soares and M.Fatima Bonaldo." BASE COUNT 95 a 121 c 84 g 102 t 3 others	Query Match 9.6%; Score 312; DB 85; Length 405; Best Local Similarity 100.0%; Pred. No. 2.9e-157; Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1262 gaaattgetggateactgecagectttggteetgacacecaateagagetgeecacatet 1321	Db 1 GAAATTGCTGGATCACTGCCCAGCTTTGGTCCTGACACCCAATCAGAGCTGCCCACATCT 60	Oy 1322 tttgctgttataacagaggatgctactttgagtccagaacttcctcctgttgaaccccag 1381	Db 61 TITGCIGITATAACAGAGGAIGCIACITIGAGICCAGAACTICCTCCTGTIGAACCCAG 120	Oy 1382 cttgagacagtggacagagcagagcatggtctacctgacacttcttggtctccacctgct 1441	Db 121 CTTGAGACAGTGGACGGAGCATGGTCTACCTGACACTTCTTGGTCTCCACCTGCT 180
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1. (bases 1 to 298)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J.F., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblow, E., Hinkle, P. S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Moreno-Palaques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrin, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Sanall, K.V., Spriggs, T.A., Utterback, T.R., Wetdman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Ferigo, D.-F., Ferile, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Intial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: arkerlavetigr.org

For clone availability, additional sequence and expression

Information related to this EST, please check the TiGR Human Gene

Index (http://www.tigr.org/tdb/hgi.html)

Seq primer: M13 Reverse.
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EST10795 Umbilical vein endothelial cells II Homo sapiens cDNA 5'
end, mRNA sequence.
AA296278
AA296278 GI:1948653
                                                                                                                                                                                                                                                                                          1526 acaatggccactgaccagacaatgctagtaccagggctcaccatccccaccagtgattat 1585
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The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
713: 3018699056
Fax: 3018699423
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/db_xref="ATCC (inhost):194417"
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/dev_stage="retina"
/dev_stage="adult"
/lab_host="Es coll strain K802"
/note="Organ: eye; Vector: lambda gt10; Site_1: EcoRI;
Site_2: EcoRI; The library used for sequencing was a sublibrary derived from a human retina cDNA library.
Inserts from retina cDNA library DNA were isolated, randomly primed, PCR amplified, size-selected, and cloned into lambda gt10. Individual plaques were arrayed and used as templates for PCR amplification, and these PCR products were used for sequencing."
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E 1 (Acses 1 to 561)

Macke, J., Smallwood, P. and Nathans, J.
Adult Human Retina cDNA

I Oppublished (1996)

On May 10, 1995 this sequence version replaced g1:805808.
Contact: Dr. Jøremy Nathans
Dr. Jøremy Nathans, Dept. of Molecular Biology and Genetics Johns Hopkins School of Medicine
725 North Wolfe Street, Baltimore, MD 21205
Tel: 410 955 4678
Fax: 410 614 0827
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//d_xref="texcon:9606"
//clone_lib-"Human retina cDNA randomly primed sublibrary"
//sex-"mixed (males and females)"
                                                                                                                                                                                                                                                                                                                                                                                                                            W26960 561 bp mRNA EST 08-MAY-1996
16h10 Human retina cDNA randomly primed sublibrary Homo sapiens
CDNA, mRNA sequence.
W26960
                                                                                                                                 1502 ctgactgatcaaggcaccacagatacaatggccactgaccagacaatgctagtaccaggg 1561
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                           1442 atggeetetacetecetgteagaagetecacetttetttatggeateaageatettetet 1501
                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
PCR PRimers
FORMARD: CITTGAGGAAGITGAGCTGGITAAGI
BACKWARD: GAGGGGCGTANGAGARITCTTCTACAGGGTAA
Seq primer: GGGTAAAAAGCAAAAGAAIT.
Location/Qualifiers
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Matches 416; Conserv
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 309)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollan,M., Rutaman,M., Rucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohling,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: estewatson.wustl.edu
Insert Size: 2489
High quality sequence stops: 106
Source: IMAGE Consortium, LLNL
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2489
Seq primer: MI3RP1
/db_xref="taxon:9606"
/clone_lib="Umbillcal vein endothelial cells II"
/cell_type="endothelial cell"
/dev_stage="fetus"
/note="Organ: umbillical vein; Vector: pBluescript SK-;
                                                                                                                                                                                                                                                                                                                                                     2939
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                                                                                                                                                                                                                                                                                                                                                                    2880 atttattgggaagcaaactctttatatgctagaaagtacatttaaaagatgactacttac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-Merck EST Project
Oppublished (1995)
On May 18, 1998 this sequence version replaced g1:3138642.
Contact: Wilson RR
                                                                                                                                                                                            ö
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H38594 309 bp mRNA EST 16-AUG
yp48c06.rl Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:190666 5', mRNA sequence.
                                                                                                                                                            Length 298;
                                                                                              2 others
                                                                                                                                                                                           Indels
                                                                                                                                                            Query Match
6.5%; Score 213; DB 24;
Best Local Similarity 99.6%; Pred. No. 1.1e-103;
Matches 263; Conservative 0; Mismatches 1;
                                                                               Site_1: EcoRI; Site_2: XhoI"
56 c 57 g 91 t
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AUTHORS
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/organism="Homo sapiens"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA326863 322 bp mRNA EST 20-APR-1997
EST3011313 Cerebellum II Homo sapiens CDNA 5' end, mRNA sequence.
AA326863 GI:1979130
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                                                                                                                                                                                                                                                                                   Length 309;
                                                                                                                                                                                                                                                                                    Query Match 5.2%; Score 168; DB 85; Length 30
Best Local Similarity 99.5%; Pred. No. 2.4e-79;
Matches 218; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1420 cacttcttggtctccacctgctatggcctctacctccct 1458
/db_xref="taxon:9606"
/clone="IMAGE:190666"
/clone_lib="Soares retina N2b4HR"
/sex="male"
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
            Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of CDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                   Bioinformatics
The Institute for Genomic Research
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699423
Fax: 3018699423
Fax: 3018699423
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/note="Organ: brain; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
88 c 70 g 85 t 5 others
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                                                                                                               On Jan 14, 1998 this sequence version replaced gi:1878018.
Contact: Kerlavage, AR
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Similarity 100.0%; Pred. No. 7.4e-73;
56; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Homo sapiens"
/db_xref-"ATCC (inhost):127542"
/db_xref-"taxon:9606"
/clone_lib-"Cerebellum II"
/tissue_type-"cerebellum"
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High Throughput Sequencing Center
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Unpublished (1997)
On May 18, 1998 this sequence version replaced gi:3138748.
On May 18, 1998 this sequence version replaced gi:3138748.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenth.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/thmi
Insert Length: 476 Std Error: 0.00
Seq primer: -400P from Gibco.
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                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/clone_llb="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Col1 DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 647;
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Exa: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2057 row: A column: 9
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.5%; Score 81; DB 95; I larity 100.0%; Pred. No. 3.1e-32; Conservative 0; Mismatches 0;
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/clone_lib="NCI_CGAP_GC6"
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/organism="Homo sapiens"
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AI632451
AI632451.1 GI:4683781
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Gaps

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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p1713 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
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NCI-GGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tunor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3188975.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royalty-ree through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 445.
                                                                                                                                                                                                                                                                                                                                   qb15b03.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696301 3' similar to contains MER18.b3 MER18 repetitive element;, mRNA sequence.
A1093483
GI:3432459
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AACTGGAAGAATTCGCGGCCGCCTTTTTTTTTTTTTTT 3'],
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                                                                                         Score 22; DB 43; Length 391;
Pred. No. 2.5;
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100.0%; Pred. No. ...
0; Mismatches
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/organism="Homo sapiens"
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/clone="IMAGE:1696301"
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/lab_host="DH10B"
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AL Unpublished (1997)

On Jun 5, 1998 this sequence version replaced gi:3189232.

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Tel: (301) 496-1550

Email: Robert_Strausberg@alh.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/Link at:

www-blo.lln.gov/Dbrp/image.html

Insert Length: 477

Seq primer: -400P from Gibco.
                                        /note="Vector: P1773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1256631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. " subtraction by 89 c 62 g 131 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jobber * Vector: P1713D-Pac (Pharmacia) with a modified polyllaker; Plasmid DNA from the normalized library NGI_CGAP_GC4 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDS 1257096-1258631, Bento Soares and M. Fatima Bonaldo."
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ts87b06.xl NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2238227 3',
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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100.0%; Pred. No. 2.5;
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AI695882.1 GI:4983782
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Gaps

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

DEFINITION

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/note="vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI;
Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa.
Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,266 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW263637 606 bp mRNA EST 28-DEC-1999 xn81b12.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700863 3' similar to SW:NUPL_HUMAN P52594 NUCLEOPORIN-LIKE PROTEIN RIP ;, mRNA sequence.

AW263637 GI:6640453
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On Feb 19, 1999 this sequence version replaced gi:4146913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 21; DB 116; Length 456; 100.0%; Pred. No. 8.8; tive 0; Mismatches 0; Indels
                Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Fmail: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .456
/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence start: 36
High quality sequence stop: 411.
Location/Qualifiers
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1 (bases 1 to 503)

1 (bases 1 to 503)

1 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP), On Jun 15, 1998 this sequence version replaced gi:3225011.

2 On Jun 15, 1998 this sequence version replaced gi:3225011.

2 Contact: Robert Strausberg@nih.gov

Toli (301) 496-1550

Email: Robert_Strausberg@nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lange.llnl.gov) for further information.

Seq primer: -400P from Gibco High quality sequence stop: 463.

Location/Qualifiers
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1 (bases 1 to 456)
Wing,R.A. and Dean,R.A.

7 BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
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    xv19d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2813569 3' similar to contains Alu repetitive
element;contains MER18.b3 MER18 repetitive element ;, mRNA
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/organism="taxon:9606"
/clone="IMAGE:2813569"
/clone=lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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VERSION KEYWORDS SOURCE

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            Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoelmage.llnl.gov) for further information.
Seq primer: -400P from Gibco
High quality sequence stop: 418.
Location/Qualifiers
1. 606
/ Organism="Homo sapiens"
/ Coganism="Homo sapiens"
/ Clone="IMAGE: 2700863"
/ Lab_host="HHGE: TGBC_SI"
/ Lab_host="HHOB"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 164)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Onpublished (1998)
Other_GSSs: RPCIII-80H22.TJ
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
seq primer: T7
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RECIII-80H22.TV RPCI-11 Homo sapiens genomic clone RPCI-11-
80H22, genomic survey sequence.
AQ284104
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Department of Eukaryotic Genomics
The Institute for Genomic Research
Tylz Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
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Best Local Similarity 100.
Matches 21; Conservative
  Unpublished (1997)
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Venter, J.C.

Was of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Other, GSSs. CITBI-E1-2506F18.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
77.1 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
and search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Ml3.21
Class: BAC ends.
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Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 228)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
BETY,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
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2506F18, genomic survey sequence.
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0; Mismatches 0; Indels
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1. 164
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Musculus; Euteleostomi; Musculus; Euteleostomi; Musculus; Euteleostomi; Mammalla; Euteleostomi; Mammalla; Euteleostomi; Masson, E. S. Kono, H., Alzawa, K., Akahira, S., Akiyama, J., Hiozaria, F., Hara, A., Hayatu, N., Hiozaria, F., Endo, T., Fukuda, S., Fukuchi, N., Fara, A., Koya, S., Kusakabe, M., Mati, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Oda, M., Carto, Matsuyama, T., Santo, M., Sato, M., Sato, K., Shipata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Soqabe, Y., Sugahara, Y., Shigemoto, Y., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Vokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, Y., Genome Exploration Research Group, Life Science Tsukuba Center, Genome Exploration Research Group, Life Science Tsukuba Center, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
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URL:http://genome.rtc.riken.go.jp,
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
Transcribtional sequencing: A method for DNA sequencing using RNA
Transcribtional sequencing: A method for DNA sequencing using RNA
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Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Ormaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y., Ozawa,Y., Muramatsu,M.,
Autonated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cona cloning. Methods Enzymol. 303,
19-44 (1999)
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AV267846 RIKEN full-length enriched, adult male testis (DH10B) Mus
musculus cDNA clone 4930529A21 3', mRNA sequence.
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                              Indels
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
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                              Mismatches
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Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGACCATGTTTTTTTTTTTTVN 3'], cDNA was
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59; Length 275; DB . 29; Ouery Match

0.6%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 81

ö 0; Indels

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Gaps

Search completed: September 3, 2000, 17:40:05 Job time: 17841 sec

us-09-183-972-3.rst

Sequence:

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Copyright (c) 1993 - 2000 Compugen Ltd.
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em_htg2::*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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TESTEKMYKMSTMRRIFDLAKHRTKRSAFFPTGVKVCPQESMKQILDSLQAYYRLRVC
QEAVWEARRIFLDRIPPTGEYQDWYSICQOEFFCFDTGKNFSNSGEHLDLLQQRIKQ
RSFPDRKDEISAEKTLGEFGETIVISTDVANVSLGPFPLIFPDTLLNEILDNTINDTK
MPTTREETERPALLESGVELGYSLVNOKFKAELADSGSPYQELAGKSQLQMOKIFKR
LPGFKKIHVLGFRPKKEKDGSSSTEMQLTAIFKRHSAEAKSPASDLLSFDSNKIESEE
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DQADPCKFLACGEFAQCVKNERTEBAECRCKPGYDSQGSLDGLEPGLCGPGTKECEVL
QGKGAPCRLPDHSENQAYKTSVKKFQNQQNNKVISKRNSELLTVEYEEFNHQDWEGN"
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SMAGSEDMVRHLDEMDLSDTPAPSEVPELSEYVSVPDHFLEDTTPVSALQYITTSSWTI
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AF017762.1:112. .278,AF017763.1:82. .110,
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AF017766.1:163. .303,AF017767.1:96. .154,
AF017768.1:153. .173,AF017767.1:96. .154,
AF017770.1:148. .224,AF017771.1:271. .349,
AF017772.1:144. .676,AF017771.1:111. .330,
AF017772.1:144. .676,AF017773.1:111. .330,
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/protein_id-"AAC68835.1"
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St. (bases 1 to 1235)
Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. and Weber, B.H.F.
Assessment of a novel interphotoreceptor matrix gene (IPM150)
localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDR1)
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AFO17762.1:1. 422,AFO17763.1:1. 300,AFO17764.1:1. 304,

AFO17765.1:1. 311,AFO17766.1:1. 377,AFO17767.1:1. 300,

AFO177768.1:1. 294,AFC017769.1:1. 444,AFO17770.1:1. 347,

AFO17771.1:1. 438,AFO1772.1:1. 816,AFO17773.1:1. 448,
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AF017764.1:107. .171,AF017765.1:139. .242,
AF017766.1:163. .303,AF017767.1:96. .154,
AF0177701:1448. .224,AF017771.1:271. .349,
AF0177701:1448. .224,AF017771.1:171. .339,
AF0177701:1448. .676,AF017773.1:111. .330,
AF017774.1:71. .269,AF017773.1:111. .330,
AF01774.1:71. .269,AF017775.1:94. .166,413. .>490)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 10 1235)
Felbor, U., Gehrig, A., Sauer, C.G., Marquardt, A., Kohler, M.,
Schmid, M. and Weber, B.H.
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Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. and Weber, B.H.F.
Assessment of a novel interphotoreceptor matrix gene (IPM150)
localized to G an autosomal dominant Stargardt-11ke
macular dystrophy, progressive bifocal chorioretinal atrophy
(PBCRA), and North Carolina macular dystrophy (MCDR1)
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Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
Direct Submission
Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg, D-97074, Germany
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Best Local Similarity 100.0%; Pred. No. 2.9e-284;
Matches 534; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/chromosome="6"
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Homo sapiens
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Lirect Submission

AL Submitted (22-Mx-2000) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

On Mar 6, 2000 this sequence version replaced gi:7009540.

IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in
progress and the release of this data is based on the understanding
that the sequence may change as work continues. The sequence may
be contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
contig_ID: 00151 Length: 8447bp
Contig_ID: 00275 Length: 8447bp
Contig_ID: 00377 Length: 1124bp
Contig_ID: 00377 Length: 1165bp
Contig_ID: 00377 Length: 3565bp
Contig_ID: 00377 Length: 2886bp
Contig_ID: 00414 Length: 1553bp
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 194704)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 TITATGGCATCAAGCATCTTCTCTGACTGATCAAGGCACCACAGATACAATGGCCACT
                                                                                                                                                                                                                                                                                                         1598 caactggctctgggaatttcacatccacctgcatcttcagatgacagccgatcaagtgca
                                                                                                                                                                                                                                                                                                                                   323 CAACTGGCTCTGGGAATTTCACATCCACCTGCATCTTCAGATGACAGCGGATCAAGTGCA
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AL157379.2 GI:7159486
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Contig_ID: 009109 Length: 21204bp
Contig_ID: 00915 Length: 6805bp
Contig_ID: 00912 Length: 6805bp
Contig_ID: 00932 Length: 10010bp
Contig_ID: 00934 Length: 10010bp
Contig_ID: 01026 Length: 2716bp
Contig_ID: 01069 Length: 2716bp
Contig_ID: 01069 Length: 2716bp
Contig_ID: 01121 Length: 10059bp
Contig_ID: 01186 Length: 10059bp
Contig_ID: 01186 Length: 1779bp
Contig_ID: 01186 Length: 1779bp
Contig_ID: 01186 Length: 1640bp
Contig_ID: 01370 Length: 1640bp
Contig_ID: 01386 Length: 1640bp
Contig_ID: 01386 Length: 1640bp

* NOTE: This is a 'working draft' sequence. It currently
consists of 28 contigs. The true order of the piecess
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the axact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              618 74.7: gap of 6617 bp in length 6618 74.7: gap of 800 bp 74.8 15.5 1664: contig of 8447 bp in length 1586 1664: gap of 800 bp 1665 18537: contig of 1847 bp in length 1838 1337: gap of 800 bp 2618 1838 26186: contig of 6849 bp in length 2618 26180: contig of 800 bp 2698 28110: contig of 1244 bp in length 2811 28940: gap of 800 bp 2891 32475: contig of 3565 bp in length 32476 33275: gap of 800 bp 3377 33275: gap of 800 bp 33276 38322: contig of 5047 bp in length 38322: gap of 800 bp
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60308: contig of 15535 bp in length
61108: gap of 800 bp
81103: contig of 19995 bp in length
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114138: contig of 12763 bp in length
114938; gap of 800 bp
138142: contig of 23204 bp in length
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184556: contig of 10059 bp in length
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138943 146423: contig of 7481 bp in length
146424 147223: gap of 800 bp
154029 154628: contig of 6805 bp in length
154029 155288: contig of 1460 bp in length
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170614: contig of 2716 bp in length
171414: gap of 800 bp
173597: contig of 2283 bp in length
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91019: contig of 7288 bp in length
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18457 18536; gap of 800 bp
185357 187387; contig of 2031 bp in length
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 444).
Felbor, U., Gehrid, A., Sauer, C.G., Marquardt, A., Kohler, M., Schnid, M. and Weber, B.H.
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187388 188187: gap of 800 bp
188188 189966: contig of 1779 bp in length
189967 190766: gap of 800 bp
190767 192406: contig of 1640 bp in length
193207 194704: contig of 1498 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                               Query Match 16.4%; Score 534; DB 32; L
Best Local Similarity 100.0%; Pred. No. 2.3e-284;
Matches 534; Conservative 0; Mismatches 0;
                                                                                                                                                                                                 /clone_lib="RPCI-1"
a 32672 c 33519 g 53383 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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Cytogenet. Cell Genet. 98358139
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 537)
Felbor, U., Gehrig, A., Sauer, C.G., Marquardt, A., Kohler, M.,
Schmid, M. and Weber, B.H.
Genomic organization and chromosomal localization of the
interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate
for 6q-linked retinopathies
Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate for 6q-linked retinopathies
                                                                               2 (bases 1 to 444)
Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E.
and Weber, B.H.F.
                                                                                                                         Assessment of a novel interphotoreceptor matrix gene (IPM150) localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI) unpublished a (barrent Carolina macular dystrophy (MCDRI) below. Unpublished a (barrent Carolina macular dystrophy (MCDRI) below. U. Kuehn, M. Hageman, G.S. and Weber, B.H.F. Submission Submitted (09-40G-1997) Humangenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg b-97074, Germany Location/Qualifiers
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Homo sapiens interphotoreceptor matrix gene (IPM150), exon 2.
AF017761-1--GEA3800716
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                                              Cytogenet. Cell Genet. 81 (1), 12-17 (1998) 98358139
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/organism="Homo sapiens"
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/chromosome="6"
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92. .339
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Submitted (12-MAR.2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
nequests: clonerequest@sanger.ac.uk
On Mar 6, 2000 this sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is unforces and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coll, yeast, vector, phage etc. Order of segments is not known; 800 n's separate
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                                               Gehrigo, A. Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. and Weber, B.H.F. and Neber, B.H.F. and Neber, B.H.F. and vel interphotoreceptor matrix gene (IPM150) localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 194704)
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E-Blobr,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.
Direct Submission
Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am
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81 (1), 12-17 (1998)
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Location/Qualifiers
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97. .330
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Homo sapiens chromosome 6 clone RF
PROGRESS ***, 28 unordered pieces.
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contig_ID: 00766 Length: 1115bp
contig_ID: 00766 Length: 1115bp
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7418 15864: contig of 8447 bp in length
15865 16664: 9ap of 800 bp
16665 18537: contig of 1873 bp in length
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40287: contig of 1165 bp in length
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82931: contig of 1028 bp in length
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60308: cont
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81103: cont
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Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E.
and Weber, B.H.F.
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Homo sapiens interphotoreceptor matrix gene (IPM150), exon 14.
AF017773.1 GI:3800728
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1 (bases 1 to 448)
Felbor, U., Gehrig, A., Sauer, C.G., Marquardt, A., Kohler, M., Schmid, M. and Weber, B.H.
Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candifor Gelinked retinopathies
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 tttggcaaagcatcgaacaaaaagatccgcatttttcccaacgggggttaaagtctgtcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 194704
                                                                                                                                                                                                                                * 185357 187387: contig of 2031 bp in length

* 187388 188187: gap of 800 bp

* 187388 188187: gap of 800 bp

* 188188 189966: contig of 1779 bp in length

190767 192406: contig of 1640 bp in length

192407 193206: gap of 800 bp

192407 193206: gap of 800 bp

192407 193206: contig of 1498 bp in length.

Location/Qualifiers
                                                                        167099 167898: gap of 800 bp 167899 170614: contig of 2716 bp in length 170615 171414: gap of 800 bp 171415 173697: contig of 2283 bp in length 173698 174497: gap of 800 bp 173698 174497: gap of 800 bp 174498 184555: contig of 1059 bp in length 184557 185556: gap of 800 bp 185557 185556: gap of 800 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53383 t 21602 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                       156288; contig of 1460 bp in length
7088: gap of 800 bp
167098: contig of 10010 bp in length
800 bp
1460 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.2%; Score 236; DB 32; L
100.0%; Pred. No. 4.7e-119;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .194704
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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/clone_lib="RPCI-1"
32672 c 33519 g
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MEDLINE
REFERENCE
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Gaps

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2 (bases 1 to 477)

Gehrig,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.E. and Weber,B.H.F.

Assessment of a novel interphotoreceptor matrix gene (IPM150)

localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate for 6q-1inked retinopathies
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Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
Flanct Submission
Submitted (09-406-1997) Humangenetik, Universitaet Wuerzburg, Am
Hubland, Wuerzburg D-97074, Germany
Location/Qualifiers
                        Universitaet Wuerzburg, Am
                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 AGIGIGICAGGAAGCAGIAIGGGAAGCAIAICGGAICTITCIGGAICGCAICCCIGACAC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSIMPGIS 477 bp DNA PRI 28-OCT-1998
Homo sapiens interphotoreceptor matrix gene (IPM150), exon 15.
AF017774
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                                                                                                                                                                                                                                                                                              Similarity 100.0%; Pred. No. 8.7e-82; 59; Conservative 0; Mismatches 0;
    Direct Submission
Submitted (09-AUG-1997) Humangenetik,
Hubland, Wuerzburg D-97074, Germany
Location/Qualifiers
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                                                                              1. .422

^^0_ganlsm="Homo saplens"

/db_xref="taxon:9606"

/chromosome="6"

/map="6q14.2-q15"

112. .278

/gene="IPM150"
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/db_xref-"taxon:9606"
/chromosome-"6"
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/gene="IPM150"
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1 (bases 1 to 423)

1 (bases 1 to 423)

Schmid,M. and Weber,B.H.
Schmid,M. and Weber,B.H.
Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate for 6q-linked retinopathies
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
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Assessment of a novel interphotoreceptor matrix gene (IPM150)
localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI)
Assessment of a novel interphotoreceptor matrix gene (IPM150) localized to 6914.2-915 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDR1) Unpublished 3 (bases 1 to 448) a (bases 1 to 448) Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F. Direct Submission Submitted (109-40G-1997) Humangenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2011 cagaaacgggaqtgtgattgtgaatagcaaaatgaagtttgctaagtctgtgccgtataa 2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1951 gctggttccatatctacgatccaatcttacaggatttaagcaacttgaaatacttaactt 2010
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Homo sapiens interphotoreceptor matrix gene (IPM150), exon 3.
RE012762
AF0134262 AF0134800717
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.2%; Score 170; DB 11; Length 448; Best Local Similarity. 99.5%; Pred. No. 2.4e-82; Matches 220; Conservative 0; Mismatches 1; Indels
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Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
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                                                                                                                                                                                                                 1. .448
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                            /map="6q14.2-q15"
111. .330
/gene="IPM150"
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DEFINITION
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/codon_start=1
/product="interphotoreceptor matrix proteoglycan 150"
/product="interphotoreceptor matrix proteoglycan 150"
/product=104="interphotoreceptor matrix proteoglycan 150"
/db_xref="GI:2906230"
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/db_xref="GI:2906230"
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/db_xref="GI:
                                                                                                                                                                                                                                                                                                                                    AF047491 555 bp mRNA PRI 24-FEB-1998 Macaca fascicularis interphotoreceptor matrix proteogilycan-150 mRNA, partial cds. AF047491
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Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-FEB-1998) Ophthalmology and Visual Sciences, University of Iowa, 200 Hawkins Drive, 11190E PFP, Iowa City, IA 52240, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kuehn, M.H. and Hageman, G.S.
Characterization And Complete cDNA Sequence Of IPM 150, A Novel
Human Photoreceptor Cell-Associated Chondroitin-Sulfate
                          400 cagtetteaagettattatagattgagagtgtgteaggaageagtatgggaageatateg 459
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100.0%; Pred. No. 3.6e-50;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .555...
/organism="Macaca fascicularis"
/db_xre="taxon:9541"
/tissue_type="retina"
<1. .>555
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Kuehn, M.H. and Hageman, G.S.
Direct Submission
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Macaca fascicularis
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Kuehn, M.H. and Hage
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Matches 112; Conservative
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Unpublished
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Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E.
and Weber, B.H.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 (bases 1 to 377)
Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
Direct Submission
Submitted (pg-AuG-1997) Humangenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany
Location/Qualifiers
                                                                                                                                                                                                                        2169 cagetgateaageagateeetgeaagtteetggeetgeggegaatttgeeeaatgtgtaa 2228
                                                                                                                                                                                                                                                                                                                                       2229 agaacgaacggactgaggaagcggagtgtcgctgcaaaccaggatatgacagccagggga 2288
                                                                                                                                                                                                                                                              68 CAGCTGATCAAGCAGATCCCTGCAAGTTCCTGGCCTGCGGCGAATTTGCCCCAATGTGTAA 127
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 377)
Felbor, U., Gehrig, A., Sauer, C.G., Marquardt, A., Kohler, M.,
Schmid, M. and Weber, B.H.
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Homo sapiens interphotoreceptor matrix gene (IPM150) → exon
AF017766
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100.0%; Pred. No. 3e-66;
ive 0; Mismatches 0; Indels
                                                                                                            Length 477;
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                                                                                                            Query Match 4.7%; Score 153; DB 11;
Best Local Similarity 100.0%; Pred. No. 6.5e-73;
Matches 153; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/chromosome="6"
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163. .303
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/gene="IPM150"
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS SEGMENT

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/organism-"Homo sapiens"
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1 (bases 1 to 438)

1 (bases 1 to 438)

Schmid, M. and Weber, B.H.

Schmid, M. and Weber, B.H.

Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate for 6q-linked retinopathies

Cytogenet. Cell Genet. 81 (1), 12-17 (1998)

98358139

2 (bases 1 to 438)
                                                        Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla; Butherla; Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 311)
Felbor, U., Gehrig, A., Sauer, C.G., Marquardt, A., Kohler, M.,
Genomic organization and chromosomal localization of the
interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate
for 6q-linked retinopathies
Gytogenet. Cell Genet. 81 (1), 12-17 (1998)
                                                                                                                                                                                                                                               Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. and Weber, B.H.F.
Assessment of a novel interphotoreceptor matrix gene (IPMI50)
localized to Gel A. 2-qi5 in autosomal dominant Stargardt-like
macular dystrophy, progressive bifocal chorioretinal atrophy
(PBCRA), and North Carolina macular dystrophy (MCDRI)
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Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
-Direct Submission
Submitted (0072406-1997) Humangenetik, Universitaet Wuerzburg, Am
Hubland, Wuerzburg D-97074, Germany
Location/Qualifiers
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Homo sapiens interphotoreceptor matrix gene (IPM45097-EXON 12.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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139. .242
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Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. and Weber B.H.F.
Assessment of a novel interphotoreceptor matrix gene (IPM150) localized to 6q.4.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI) Unpublished

I. Unpublished

S. Felbor, U., Kuchn, M., Hageman, G.S. and Weber, B.H.F.
Direct Submission

Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany

Location, Qualifiers
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Assessment of a novel interphotoreceptor matrix gene (IPM150)
Assessment of an autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI)
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Direct Submission
Submitted (199-40-1997) Humangenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 347)
Felbor,U., Gehrig,A., Sauer,C.G., Marquardt,A., Kohler,M.,
Schmid,M. and Weber,B.H.
Genomic organization and chromosomal localization of the
interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candifor 6q-linked retinopathles
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
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2.5%; Score 81; DB 11; I
Best Local Similarity 100.0%; Pred. No. 5.6e-33;
Matches 81; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/chromosome="6"
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Search completed: September 3, 2000, 16:29:14 Job time: 21871 sec

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DNA encoding rat H
Nuclectide sequenc
Human gene signatu
EST clone B141. Ne
Tumor necrosis fac
TWF-R1-DD ligand p
Encodes human IGFB
Insulin-11ke growt
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IGFBP6 DNA. Insuli
Human insulin-11ke
Bacterial transfer
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Bacillus firmus so
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(without alignments)
707.694 Million cell updates/sec
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PaMMV coat protein
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Human proline-rich
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Encodes rat IGFBP-
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                              311585 seqs, 125096042 residues
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                                                      OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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CDNA sequence SEQ CDNA encoding gluc Human secreted pro Human FADD-interac Human FADD-interac Human EAAT5 glutam Bovine male enhanc Glucoamylase P gen Mammalian MEK kina MEKKI protein codi DNA encoding a mu MEKKI protein codi DNA encoding a Bac NTS	otein coupled receptor. or; cell differentiation; proliferation; islon; growth factor response; rat-edg; rs rs equence associated with mRNA sequence associated with mRNA loab 102b 102b 102b 103b 315h 102b) alish alish alish alish the encodes p(H218), a member superfamily of proteins. The amino acid (W01664) suggests that endogenous ligand(s). The expression th genes in cell lines, various rat suggests that they both play a role in nitation. 714 G; 677 T; e 18; DB 1; Length 2754;
X19251 T90830 X00649 X08909 X19248 Q79135 Q79135 T90831 Q79325 T05570 V22676 V45619 V16518	54 BP. 18), G-protein coupled ed receptor; cell diffication; growth and in the coll division; growth and in the coll division; growth and consensus sequence assign; 248 248 248 397 bentiation 397 consensus sequence assign; 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026) 1026)
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WPI, 95-206931/27.
          Dolganov G;
WPI; 97-393672/36.
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                                                     homologues
                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide encoding a G-protein coupled receptor used to develop products for use in diagnosis and therapy of conditions involving cell proliferation and differentiation claim 1, Columns 15-18; 33pp; English.

The present sequence encodes a protein designated H218. The H218 polypeptide is a member of the G-protein coupled receptor superfamily. The H318 polypeptide is involved in cell proliferation and differentiation, and in disease states such as cancer. The
                                                                                                                                        12-MAR-1999 (first entry)
DNA encoding rat H218, G-protein coupled receptor superfamily member.
H218; G-protein coupled receptor superfamily; cell proliferation;
cell differentiation; cancer; diagnosis; therapy; ss.
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-DEC-1998 (first entry)
Nucleotide sequence encoding human RAD50 exon 11.
ds; human; RAD50; DNA repair; tumour suppression; cancer; Septin-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotides and polypeptides can be used to develop products
                                                                                                                                                                                                                                                               sequence associated with mRNA
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        Pred. No. 7.
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//note= consensus sequinty=
                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.2.,
100.0%; Pre-
100.08; Pr
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/product= H218
2393. .2397
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T75262/C

ID 75262 standard; DNA; 158 BP. AC T75262;
DT 21-DEC-1998 (first entry)
DE Nucleotide sequence encoding hu
KW ds; human; RAD50; DNA repair; t
KW central nervous system.
OS HOMO sapiens.
PN W09727284-A2.
PD 31-UUL-1997.
PF 24-JAN-1997; U01299.
PR 24-JAN-1996; US-687080.
PR 26-JAN-1996; US-687080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for diagnosis and therapy.
                                                                                                                   V84039 standard; DNA; 2754 BP
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                                         217 ttcagcaattcccaggag 234
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Best Local Similarity 100.
      Best Local Similarity 100.
Matches 18; Conservative
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06-DEC-1996; 760936.
15-FEB-1994; US-196989.
06-DEC-1996; US-760936.
                                                                                                                                                                                                                                                                                                                                                                (MACL/) MACLENNAN A J.
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 99-105192/09.
P-PSDB; W87790.
                                                                                                                           V84039;
12-MAR-1999
DNA encoding
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                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                      polyA_signal
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                                                                                The human RAD50 (hRAD50) is involved in DNA repair and has tumour suppression activity, can be used to detect predisposition to, decrease suppression activity, can be used to detect predisposition to, decrease the risk of or treat cancers, e.g. acute myeloid leukaemia, myelodysplastic syndrome, therapy related myelodysplastic syndrome, therapy related myelodysplastic syndrome, therapy related acute myeloid leukaemia, refractory anaemia or refractory anaemia with excess blasts. Also disclosed in this invention is Human Septin-2 homologues of which may be used as targets for cancer therapies and central nervous system directed treatment methods, and to measure the proliferative potential of selected cell types.
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Cauble-stranded DNA) which comprises one of the 7837 "GS" sequences given in 179001-175837 and which is able to hybridise to part of former in 179001-175837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-contranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 355 BP; 109 A; 60 C; 64 G; 118 T;
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                    predisposition to, decrease risk of and treat cancer, also Septin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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23;
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useful to detect
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23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T19541 standard; cDNA to mRNA; 355 BP.
T19541;
Human tumour suppressor gene RAD50 -
                                                                                                                                                                                                                                                                                                                                                                                                                          28 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissues
Claim 1; Page 412; 2245pp; Japanese.
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100.0%; Pr
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Human gene signature HUMGS00604.
                                                                                                                                                                                                                                                                                                                                                                                                                    69 A;
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nes 17; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
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158 BP; 69
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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DESCRIPTION OF THE PROPERTY OF

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binding - for prevention and treatment of pref. anti-inflammatory
conditions, e.g. auto-immune disease, graft versus host reaction
per conditions, e.g. auto-immune disease, graft versus host reaction
cotteoporosis, e.g.
Claim 27; Page 39-40; Bipp; English.
CC The present sequence, clone 20DD (ATCC 69704), encodes a tumour necrosis
CC factor (TNF) receptor 1 (R1) death domain (DD) ligand (see R95728). A
cyeast genetic selection method, the "interaction trap", was used to
correct this receptor 1 (R1) death domain (DD) ligand (see R95728). A
cyeast genetic selection method, the "interaction trap", was used to
corf the P55 type 1 TNF-R. The protein (895238) encoded by clone 20DD is
clone 20DD and in the protein (189528) encoded by clone 20DD is
clone 20DD and IGFBP-5, IGFBP-5 and certain fragments of it will exhibit
cord. Clone 20DD and in the prevention and treatment of anti-inflammatory
conditions and other conditions such as cachesta, autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27: Page 42-43; 103pp; English.

Claim 27: Page 42-43; 103pp; English.

This sequence represents the coding sequence of the invention. This sequence was isolated from clone 20DD and encodes a tumour necrosis and cartor receptor P55 type (TNF-R1) death domain (DD) ligand protein. A chost cell containing this sequence is used for the recombinant production of TNF-R1-DD. The TNF-R1-DD ligand protein can be used in a method to identify inhibitors of TNF-R DD binding. The TNF-R1-DD ligand protein, insulin-like growth factor binding protein-5 (IGFBP-5, has TNF-R1-DD ligand activity) or inhibitors of TNF-R1-DD ligand protein are capable of preventing or ameliorating an inflammatory condition, preferably by inhibiting TNF-R DD binding. Identification and isolation of ligands inhibiting TNF-R DD binding. Itentification and isolation of ligands therefore a silows their effects upon TNF-R signal transduction and use as therefore agained.

Examined.
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TWR-RL-DD ligand protein clone 20DD coding sequence.
Tumour necrosis factor receptor P55 type; TWR-RL-DD ligand protein;
death domain; TWR-R1; inhibitor identification; TWR-induced condition;
insulin-like growth factor binding protein-5; inflammatory condition;
IGFBP-5; therapy; ds.
HOMO Saplens.
                                                                                                                                          TNF receptor death domain ligand proteins and inhibitors of ligand binding - for prevention and treatment of pref. anti-inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour necrosis factor receptor P55 type death domain ligand proteins – useful for preventing or ameliorating inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 graft versus host reaction, osteoporosis, diabetes, etc. . Sequence 722 BP; 197 A; 228 C; 182 G; 115 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Length 722;
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100.0%; Pred. No. 23;
:ive 0; Mismatches
                                        Schievella AR
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15-AGG-1996; US-698551.
15-FEB-1996; US-602228.
GEMY ) GENETICS INST INC.
Chen J, Graham J, Lin L, Schievella AR;
WPI; 97-424976/39.
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2. .562
/*tag= a
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(GEMY ) GENETICS INST INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 GGACTGGGTCAGCTTCT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.1
Best Local Similarity 100.
Matches 17; Conservative
                                Chen J, Graham J,
WPI; 96-230551/23.
P-PSDB; R95328.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Polynucleotides encoding human secreted proteins - derived from
e.g. human blood, kidney, foetal lung, placenta, testes, brain,
e.g. human blood, kidney, foetal lung, placenta, testes, brain,
e.g. human blood, kidney, foetal lung, placenta, testes, brain,
py ovary, pituitary, retina and colon cDNA libraries
Claim 1: Page 382; 633pp; English.

This sequence represents an expressed sequence tag (EST), and is a
color cereted EST sequences isolated from a variety of human tissue
cources. The EST sequences and proteins encoded by them are predicted to
have useful biological activities which would make them suitable for
treating, preventing or ameliorating medical conditions in humans and
animals, although no supporting data is given. Suggested activities
include nutritional activity, immune stimulating or suppressing activity,
heematopoiesis regulating activity, tissue growth activity, haemostatic
activity, andhough no supporting activity, tissue growth activity, activity, receptor/ligand activity, tumour inhibition
activity, cadherin/tumour invasion suppressor activity, tumour inhibition
activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                      EST clone B141.

Est clone B141.

Est clone B141.

Est clone B141.

Lispressed sequence tag; secreted protein; haematopolesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotraxis; chemotrasis; dene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
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TNF-R1-DD; tumour necrosis factor receptor 1 death domain; inhibitor;
PS5; anti-inflammatory; autoimmune disease; graft versus host reaction;
osteoporosis; cachexia; diabetes; sequence identity; IGFBP-5;
insulin-like growth factor binding protein-5; ds.
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Pred. No. 23;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agostino MJ, Jacobs R, Lavallie ER, McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M; 99-070076/06.
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100.0%; Pre-
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                                                                                                                                                                                                                       V86891 standard; cDNA; 430 BP.
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/*tag= a
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10-APR-1997; US-835913.
(GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                            (first entry)
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19-0CT-1994; US-327514.
19-JUN-1995; US-494440.
26-SEP-1995; US-533901.
   85 AATCCATGAAACAGATT
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Best Local Similarity
Matches 17; Conserv
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WO9845435-A2.
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T15230/C T15230/C T152 DT 7152 DE 709-D ET 708-D E

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Gaps

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Lin L, Schievella AR;

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BP;
                            WPI; 96-230551/23
P-PSDB; R95328-29
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T94634/c
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This sequence encodes human insulin-like growth factor binding protein. The insert from Q28270 was excised and subsequently used as a probe to screen a human placenta cDNA library. Positive clones were prepared, purified, and one of the longest clones subcloned into pBluescript SK+
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Insulin-like growth factor binding protein-5 (IGFBP-5) cDNA.
Insulin-like growth factor becaptor 1 death domain; inhibitor;
TNR-RI-DD; tumnour necrosis factor receptor 1 death domain; inhibitor;
P55; anti-inflammatory; autoimmune disease; graft versus host reaction; osteoporosis; cachexia; diabetes; sequence identity; IGFBP-5; insulin-like growth factor binding protein-5; ds.
                                                                                                                      Gaps
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Encodes human IGFBP-5.
human insulin-like growth factor binding protein-5; IGF-I; IGF-II;
breast cancer; bone cancer; modulating bone growth; purification;
affinity columns; antibodies; diagnosis; testing; ss.
Synthetic.
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                                                    Length 722;
                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 G;
                                                        Score 17; DB 1;
Pred. No. 23;
0; Mismatches 0
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14-FEB-1991; US-658410.
(WHIT-) WHITTIER INST DIABETES & ENDOCRINOLOGY.
Ling NC, Shimaski S;
WPI, 92-316186/38.
P-PSDB; R26995.
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57. .875
/*tag= a
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57. .872
/*tag= a
                            3.1%; Sco...
100.0%; Pre
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                                                                                                                                                                           ggactgggtcagcttct 175
                                                                                                                                                                                                             232 GGACTGGGTCAGCTICT 216
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19-JUN-1995; US-494440.
26-SEP-1995; US-533901.
(GEMY ) GENETICS INST INC.
                                                        Query Match 3.1
Best Local Similarity 100.
Matches 17; Conservative
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hes 17; Conservative
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12-OCT-1995; U12724.
19-OCT-1994; US-3275
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Sequence 1023 BP;
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Productions, etc.
PS Columinations, etc.
PS Claim 27, Page 41-42; 83pp; English.
Claim 27; Page 41-42; 83pp; English.
Claim 27; Page 41-42; 83pp; English.
CC The present sequence encodes insulin-like growth factor binding protein-5 (CC R95329) and a tumour necrosis factor (TNF) receptor 1 (R1) death domain CC (DD) ligand (Colone 200D; R95328) it has been determined that IGFBP-5 and CC train fragments of it, will exhibit TNF-R1-DD ligand binding activity.
CC A yeast genetic selection method, the "interaction trap", was used to CC screen Mi38 cell cDNA libraries for proteins that interact with the DD of the P55 type 1 TNF-R. TNF-R1-DD ligands and their inhibitors, e.g.
CC offens.
CC GFRBP-5, are useful in the prevention and treatment of anti-inflammatory CC conditions and other conditions such as cachexia, autoimmune disease, CC graft versus host reaction, osteoporosis, diabetes, etc.
Sequence 1023 BP; 224 A; 352 C; 284 G; 163 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conditions
Claim 27; Page 44-45; 103pp; English.

This squence represents the coding sequence of the invention. This This squence encodes the insulin-like growth factor binding protein-5 captures a squence encodes the insulin-like growth factor binding protein-5 squence encodes the insulin-like growth factor receptor P55 type (INF-R1) captured domain (DD) ligand protein. A host cell containing this sequence is used for the recombinant production of INF-R1-DD. The INF-R1-DD ligand protein can be used in a method to identify inhibitors of TNF-R1-DD ligand protein are espable of activity), or inhibitors of TNF-R1-DD ligand protein are capable of preventing or ameliorating an inflammatory condition, preferably by inhibiting TNF-R DD binding. Identification and isolation of ligands allows their effects upon TNF-R signal transduction and use as therapeutic agents for treatment of TNF-Induced conditions to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Tumour necrosis factor receptor P55 type; INF-RI-DD ligand protein;
death domain; TNF-RI; inhibitor identification; TNF-linduced condition;
insuln-11ke growth factor binding protein-5; inflammatory condition;
IGFBP-5; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
TNF receptor death domain ligand proteins and inhibitors of ligand binding - for prevention and treatment of pref. anti-inflammatory conditions, e.g. auto-immune disease, graft versus host reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Length 1023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΰ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.1%; Score 17; DB: 100.0%; Pred. No. 23; tive 0; Mismatches
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115-AGC-1996; US-69851.
115-FEB-1996; US-60228.
(GEMI ) GENETICS INST INC.
Chen J, GRADAM J, Lin L, Schievella AR;
WPI: 97-424976/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ပဲ
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57. .875
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T94634;
19-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 17; Conservative
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226814;

RESULT 11

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PROPERTY OF TAIL OF TA
                                                                                                                                                                                                                                                                                         Andress DL, Kiefer MC;
Andress DL, Kiefer MC;
RP1; 94-16795/20.
RP5DB: R55084.
Truncated insulin-like growth factor binding protein - has reduced affinity for insulin-like growth factor, useful for steaulating bone cell growth and mitogenic activity

C This sequence is contained in plasmid pBsBP6-1A and encodes 2

C preferred truncated IGFBP-5 proteins derived from human U-2

C osteosarcoma cells. This sequence may be optionally fused to a calcitonin gene for expression in a recombinant host, preferably yeast or CHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial transferrin receptor operon (H. influenzae strain SB33).
Thpl: Thp2: transferrin receptor operon; vaccine; antigen;
non-typable strain; Haemophilus influenzae; meningitis; ss.
Haemophilus influenzae strain SB33.
Key
192. 698
192. 698
/*tag= a
/*tag= a
/note= "preferred truncated IGFBP-5, claim 12"
123. .627
                                                                             /*tag- b
/note- "preferred truncated IGFBP-5, claim 13"
63. .881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1650;
24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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100.0%; Pred. No. 24;
iive 0; Mismatches
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/*tag= b
/product= Tbp1
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Matches 17; Conservative
                                                                                                                                                                                                                                                                         US-972142.
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29-OCT-1993; U10462.
04-NOV-1992; US-9721.
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Q94446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypopitulitatism, osteoporosis, anaemia(s), cancer, etc., stimulating growth and wound healing, also useful in diagnosis claim 8 Fig1 1, 65pp; English.

CR was used to isolate insulin-like growth factor binding protein 6 (IGFBP6) from a human osteosarcoma cDNA template using PCR primers whose sequences were based on regions of high homology between the amino acid sequences of five known IGFBPs.

Two probes were synthesised, based on the sequence of the PCR prod. and were used to screen a ZAPII/human osteosarcoma cDNA library.

Two probes were synthesised, based on the sequence of the PCR prod. and were used to screen a ZAPII/human osteosarcoma cDNA library.

Two probes were synthesised, based on the sequence of the PCR prod. and were double positive clones were found and were analysed by restriction digestion. A unique sequence of ca. 1.7 kb designated IGFBP6 was identified. IGFBP6 may be used alone, or with IGF to stimulate growth, tissue or organ regeneration or wound healing. Also IGFBP6 has applications in the treatment and diagnosis of hypopitulitarism, osteoporosis, anaemias, and disorders due to excessive prodn. of free IGF, e.g. breast or kidney cancer, the binding protein can also be used too purify IGF e.g. by affinity chromatography. See also Q26810-4.
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Insulin; like; growth factor; binding protein; BP-6; IGF; growth; regeneration; hypopituitarism; oseoporosis; anaemia; breast cancer; kidney cancer; diabetic retinopathy; purification; ss. Synthetic.
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Q65519;
28-NOV-1994 (first entry)
Human insulin-like growth factor binding protein-5 DNA.
Insulin-like growth factor binding protein-5; IGFBP-5; hormone;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.1%; Score 17; DB 1; Length 1611; 00.0%; Pred. No. 24;
                           DB 1; Length 1023; 23;
     3.1%; Scc. Vo. 2., 100.0%; Pred. No. 2., ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 24;
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549. .132
                                                                                                                                                                                                                                                                                                    Q26814/c
ID Q26814 standard; DNA; 1611 BP.
                                                                                                                                       159 ggactgggtcagcttct 175
                                                                                                                                                                                           545 GGACTGGGTCAGCTTCT 529
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                                                                                                                                                                                                                                                                                                                                                                               20-JAN-1993 (first entry)
IGFBP6 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
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                              Query Match 3.1
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JAN-1992; U00107.
08-JAN-1991; US-638628.
(CHIR) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 92-268666/32.
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mat_peptide
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Gaps

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292 T;

Gaps

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Indels

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Mismatches

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17; Conservative
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V21440
     Matches
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The present sequence represents the transferrin receptor gene of Raemophilus influences type b, strain SB33. The bacterial transferrin Raemophilus influence type b, strain SB33. The bacterial transferrin receptor is composed of 2 chains, Typl and Thp2. Hinfluencae is a non-encapsulated or non-typable bacterium responsible for a wide range of human diseases. Iron is an essential nutrient for the growth of these control of the access of the transferrin as a source of iron. Antibodies which block the access of the transferrin receptor to its iron source prevent bacterial growth. The transferrin receptor, or fragments, therefore, are good vaccine candidates. The full length Thp2 protein is produced in low amounts in Escherichia coli. However, the yield can be enhanced by truncation of the 3' end of the gene. An immunogenic composition comprising (or encoding) the immunogenic caused by a bacterial pathogen that produces the transferrin receptor. The immunogenic truncated analogue is also useful as an anique in the immunogenic truncated analogue is also useful as an anique in
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tbp2. Antibodies blocking this binding site may prevent bacterial growth. Fragments of the TfR (or its genes) are useful in vaccines to provide protection against, e.g. bacterial meningitis. An advantage of using the TfR is that it shares homology with TfR of other H. influenzae strains including non-typable strains.

Sequence 5144 Bp; 1813 A; 888 C; 973 G; 1470 T;
                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferrin receptor gené sequence encoding Tbpl and Tbp2.
Transferrin receptor; Haemophlius influenzae type b;
Tron; human transferrin; iron source; antibody; bacterial growth;
vaccine; immunogenic truncated analogue; antigen; Tbp1; Tbp2; ss.
Haemophlius influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus truncated transferrin receptor protein analogue, Tby
used to induce protection against disease caused by transferrin
producing pathogens, or as antigen to detect Haemophilus TfR
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                                                                                                                                                                                                                     DB 1; Length 5144; 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-1996; US-649518.
07-JUN-1995; US-483577.
(CONN-) CONNAUGHT LAB LTD.
Chong P, Gray-Owen S, Harkness RE, Klein MH, Loosmore SM,
Murdin AD, Schryvers AB, Yang Y;
                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192. .698
/*tag- a
/note- "encodes Tbp2 (W08966)"
2135. .4870
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/note= "encodes Tbp1 (W08965)"
                                                                                                                                                                                                                                                                           Mismatches
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Pred. No.
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                                                                                                                                                                                                                     Query Match 3.1%; Sc
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                454 gaaagagaaacagaact 470
                                                                                                                                                                                                                                                                                                                                                               929 GAAAGAGAAACAGAACT 945
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07-JUN-1996; CA0399.
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P-PSDB; W08965-66
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1149504
AC 749504
AC 749504
DT 74904

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DB 1; Length 5144; 24;

3.1%; Score 17; 100.0%; Pred. No.

Query Match Best Local Similarity

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Purification of recombinant Haemophilus transferrin-binding protein purification of recombinant Haemophilus transferrin-binding protein by solubilising inclusion bedies separated from cell lysate Example 4; Fig 7; 261pp; Engalish.

The H. influenzae transferrin receptor operon contains two genes (tbpl and thep) under the transcriptional regulation of one promoter. The proteins encoded from these genes can be expressed in a recombinant host. The proteins can be used in vaccines against H. influenzae infections or to produce antibodies for use in diagnosis or passive
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                                                                                                                                                                                     20-JUL-1998 (first entry)
H. influenzae strain SB33 transferrin receptor operon.
tbp1; tbp2; vaccine; H. influenzae; antibody; diagnosis; passive immunisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JAN-1998.

13-JAN-1998.

07-JUN-1994; US-337483.

08-NOV-1993; US-148968.

29-DEC-1993; US-175116.

07-JUN-1995; US-478890.

CONN-) CONNANGHT LAB LID.

CONN-) CANANGHT LAB LID.

CONN-) GIRAY-OWEN S, HAIKNESS R, Klein M, LOOSMOIE S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             974 G;
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Pred. No.
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192. .698
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2135. .4870
/*tag= h
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                                                                                                                                               V21440 standard; cDNA; 5144 BP. V21440;
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100.0%;
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454 gaaagagaaacagaact 470
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Best Local Similarity 100.
Matches 17; Conservative
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Job time: 13489 sec
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Query Match
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4158.179 Million cell updates/sec
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Encodes Taf DNA po
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Mutant thermostabl
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Human mGluR7 clone
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1 taaaccaagaaggttatcct......tactatatgacataatcaat 3261
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                            311585 seqs, 125096042 residues
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V20441
X20248_00
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                                     OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Q24331
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X07172
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Q71390
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Maximum DB seq length: 1000000
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0.5 752 1 V53451 DNA encoding a Sta 0.5 920 1 Q22366 MAGE-10 genomic DN 0.5 920 1 Q72491 TO120 G.5 1099 1 Q25831 MAGE-10 geno. Dete 0.5 1101 1 N90131 DNA sequence of pB 0.5 1101 1 N90135 DNA sequence of pB 0.5 1101 1 N90345 Plasmid pBSF2-18, Plasmid pBSF2-18, 0.5 1101 1 N81517 Sequence encoding 0.5 1128 1 Q74057 Human interleukin 0.5 1128 1 V60294 Human interleukin	ALIGNMENTS	dard; cDNA; 1399 BP.	4644		9 9	ם ע	/*tag= /note= in the ce 985	/*tag= /note= in the ce 1090	/*tag= 1 /note= "base n at position 1090 is not identified in the specification"	(Q <del>-VAR-1995)</del> 07-SEP-1994; EP-810663. 20-SEP-1993; EP-810663. 19-Aug-1994, GB-016553.	) CIBA GEIGY AG. PJ. Knoepfel T. Kuhn R. Lindauer K. Puettner I; PS-139596/18.	094.  Outropic glutamate receptor sub-type(s), esp. 4, 6 and rresp. DNA and antibodies, useful for identifying modulate signal transduction activity age 62-64: 110pp:	tropic glutamate receptor subtype 7 (hmGluR7) isolated from cDNA libraries using a rat mGluR partial cDNA clone cmR3, encoding the protein obtained. The missing 5' region of the clone pocampus clones indicated the existence of 2: R72097-98).	366
111111111111111111111111111111111111111		standard;		, .	ifferen	feren	ifferen	differenc	627-A.	-1995. -1994; E -1993; E	) CIBA G J, Knoe 5-139596	n metabotropion also corresp.  which modula n 17: Page 62:	man metaboticones were is lppocampus pa 12094, was ob enerated by I ain and hipp	<b>~</b>
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Length 1399;

DB 1;

0.6%; Score 20;

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2568 BP;
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30-SEP-1991; (28-SEP-1990; (
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028937/c
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Claim 11; Page 59; 185pp; English.

The sequence is that of Thermosipho africanus polymerase DNA which has been mutated. The mutation designated prail causes the polymerases are useful in many recombinate DNA techniques, esp.

C polymerases are useful in many recombinant DNA techniques, esp.

Ducletc acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' unclease activity may facilitate higher sensitivity allelic 5'-3' another action in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and encoding particular regions of the enzymes can be used to prepare a recombinant proteins having 5'-3' exonuclease activity
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024331,
22-0CT-1992 (first entry)
Mutant thermostable DNA polymerase pTAF09.
5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss.
                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "nucleotides 4-417 deleted from the native
                                                                                                                                                                                                                                                22-071-1992 (first entry)
Mutant thermostable DNA polymerase pTAF11.
5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR;
Thermosipho africanus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              688 T;
                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to a complete lack of activity.
See also Q23993-Q24013, Q24320-36 and Q24343-60.
  Pred. No. 5.2;
                       Mismatches
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                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                              RESULT 2
024332,
DG74332 standard; DNA; 2265 BP.
CG24332;
DT 22-OCT-1992 (first entry)
DE Mutant thermostable DNA polymera
KW 5'-3', exonuclease; PCR; amplific
ST Thermoslpho africanus.
FT Key
FT (1d_sequence 1...2
FT (1d_sequence 1...3
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                                                          3112 aataatctttgaattgttct 3131
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100.08;
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Best Local Similarity 100.
Matches 20; Conservative
                     Conservative
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  Best Local Similarity
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old_sequence
                       20;
                     Matches
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Trible having conserved regions mutated or deleted, for use activity - having conserved regions mutated or deleted, for use activity - having conserved regions mutated or deleted, for use in the activity - having conserved regions mutated or deleted, for use claim 11; Pages 59; 185pp; English.

The sequence is that of Thermosipho africanus polymerase DNA which has been mutated. The mutation designated pTAR09 causes the polymerases are useful in many recombinant DNA techniques, esp. polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic collistration in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity collistrate lack of activity.

Los complete lack of activity.

See also Q23993-Q44013, Q24320-36 and Q24343-60.

Sequence 2403 BP; 947 A; 257 C; 467 G; 732 T;
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/*tag= a
/note= "nucleotides 4-279 deleted from the native
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Encodes Taf DNA polymerase I lacking 5'-3' exonuclease activity.
Thermostability; PCR; polymerase chain reaction;
thermophilic bacteria; Taf Pol I; deletion mutant; ss.
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26-SEP-1991; UG-590490.
28-SEP-1990; UG-590490.
(CETU ) CETUS CORP.
Abramson RD, Gelfand DH, Greenfleld L, Lawyer FC, Reichert FL;
WPI; 92-150887/18.
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                                                                    sequence.
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Matches 20; Conservative
                                                                                                                                                                     30-SEP-1991; U07035.
28-SEP-1990; US-590213.
28-SEP-1990; US-590466.
28-SEP-1990; US-590490.
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WPI; 92-150885/18
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RESULT

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Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays

Claim 11; Page 59; 185pp; English africanus polymerase DNA which has been mutated. The mutation causes the polymerase enzyme produced to exhibit a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, salf-sustained sequence replication (SSR) and high temp. DNA equencing. The absence replication (SSR) and high temp. DNA equencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
Second 223993-Q24013, Q243120-36 and Q24343-60.
Sequence 2679 BP; 1045 A; 295 C; 515 G; 824 T;
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Encodes App37 Taf DNA polymerase I lacking 5'-3' exonuclease activity.
Thermostability; PCR; polymerase chain reaction;
thermophilic bacteria; Taf Pol I; mutant; ss.
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26-SEP-1991; UO7076.
28-SEP-1990; US-590490.
(CETU ) CETUS CORP.
Abramson RD, Gelfand DH, Greenfield L, Lawyer FC, Reichert FL;
WPI; 92-150887/18.
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/note= "Gly codon changed to Asp"
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/note= "A in native sequence"
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                 Location/Qualiflers
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Q28936/c
ID Q28936 standard; DNA; 2679 BP.
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                                                              /*tag=
/note=
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28-SEP-1990; US-590213.
28-SEP-1990; US-590466.
28-SEP-1990; US-590490.
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  Thermus thermophilus.
                                                                                                                                                                                                                                                                                                      CETU ) CETUS CORP
                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R23169
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                                          old_sequence
                                                                                                           old_sequence
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                                                                                                                                                                       WO9206200-A.
                                                                                                                                                                                           16-APR-1992
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Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use activity - having conserved regions mutated or deleted, for use in e.g. PCK. sequencing and detection assays

Claim 11: Page 59: 185pp; English.

The sequence is that of Thermosipho africanus polymerase DNA which has been mutated. The mutation designated prafeta's rauses the polymerases enzyme produced to exhibit a different ant. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity as lealing also assay. An enhanced ant. of 5'-3' exonuclease activity may be desirable alsorimination in a combined polymerase ligase chain reaction (BLCR) assay. An enhanced ant. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a region of a parget in the prompting of the enzymes can be used to prepare
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                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                    22-007-1992 (first entry)
Mutant thermostable DNA polymerase pTAFd2-37.
5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               024329/c
ID 024329
AC 024329.
DT 22-OCT-1992 (first entry)
DE Mutant thermostable DNA polymerase from Thermosipho africanus.
KW 5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss.
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1. .2
/notes a nucleotides 4-111 deleted from the native
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                                     Length 2568;
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                                                                                    0; Indels
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                                        DB 1;
5.2;
                                        0.6%; Score 20; DB
100.0%; Pred. No. 5.2
ative 0; Mismatches
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                                                                                                                          to a complete lack of activity
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                                                                                                                                                                                                                                                                                Q24330 standard; DNA; 2571 BP
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28-SEP-1990; US-590213.
28-SEP-1990; US-590466.
28-SEP-1990; US-590490.
(CETU ) CETUS CORP.
Abramson RD, Gelfand DH;
WPI; 92-150885/18.
P-PSDB; R23170.
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Best Local Similarity 100.'
Matches 20; Conservative
                                          Query Match 0.69
Best Local Similarity 100.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Thermosipho africanus.
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RESULT

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Gaps

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Query Match
Best Local Similarity
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                                                                                     Matches
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Q23917/
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                                                                                                                                                                                                                                                                                Gaps
               The sequence coding for a thermostable DNA polymerase was isolated from chromosomal DNA of Thermosipho africanus (Taf). The polymerase (see R23122) has 5'-3' exonuclease activity. Mutation of the codon specifying Gly at position 37 (i.e. GGA) to an Asp codon results in a DNA polymerase which lacks the 5'-3' exonuclease activity. See Q23917 for the wild-type Taf Pol I gene and Q28937 for another preferred mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and 7 - also corresp. DNA and antibodies, useful for identifying cycls. Wich modulate signal transduction activity claim 17, Page 49-56, 110pp; English.

Human metabotropic glutamate receptor subtype 7 (hmGluR7) cDNA clones were isolated from cDNA libraries using a rat mGluR4 probersetal brain partial cDNA clone cRR2, encoding the protein given in R72093, was obtained. The missing 5' region of the clone was generated by PCR from brain cDNA. Sequence comparison of fetal brain and hippocampus clones indicated the existence of 2 subtypes of hmGluR7 (R72097-98).
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/note= "base n at position 3325 is not identified
in the specification"
3346
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/note- "base n at position 3351 is not identified
in the specification"
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Human metabotropic glutamate receptor subtype 4; mGluR7; hmGluR7; signal transducer; ss.
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in the specification"
3494
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                                                                                                                                                                        823 T;
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5.2;
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/note= "base n at position 3346 is not
in the specification"
3351
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in the specification"
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19-AUG-1994; GB-016553.
(CIBA) CIBA GEIGY AG.
WPI; 95-139596/18.
                                                                                                                                                                                                                                 0.6%; Score 20; DB 100.0%; Pred. No. 5.2 Live 0; Mismatches
                                                                                                                                                                      295 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               892 C;
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1. .2604
Page 70; 80pp; English
                                                                                                                                                                      1045 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q89343 standard; cDNA; 3804 BP
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"base
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3325
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Best Local Similarity 100.0
Matches 20; Conservative
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3804 BP;
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                                                                                                                                                                        2679 BP;
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07-SEP-1994; E02991.
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26-SEP-1995
  Claim 20;
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Q89343
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Thermostable DNA polymerase from Thermosipho africanus - prepd.

Thermostable DNA cells or by expression of Taf polymerase gene in host cells

Claim 8; Page 6; 80pp; English.

Chromosomal DNA from Thermosipho africanus (Taf) was PCR-amplified with degenerate primers corresponding to the amino acid sequences of conserved regions of known thermostable polymerases. When specific PCR products of a similar size to the product generated using Tag chromosomal DNA were produced, the PCR fragments were cloned and sequenced. Fragments with sequences which encoded regions of amino acid homology to known thermostable polymerases were identified. The cloned PCR products were used as probes to screen a genomic Southern blot. The full-length Taf coding sequence was then compiled from various clones. See also Q23918-Q23961.
                                                        Gaps
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Diaminopimelate epimerase; soybean; amino acid; lysine;
threonine; methionine; cysteine; isoleucine; transgenic plant;
crop improvement; food; feedstuff; ss.
Glycine max.
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28-SEP-1990; US-590490.
(CETU ) CETUS CORP.
Abramson RD, Gelfand DH, Greenfield L, Lawyer FC, Reichert FL;
WPI: 92-150887/18.
P-PSDB; R23122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 4286; 5.2;
Length 3804;
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                                                                                                                                                                                                                                                                                                                                                              Taf DNA polymerase I coding sequence. Thermostability; PCR; polymerase chain reaction; thermophilic bacteria; Taf Pol I; ss.
     DB 1;
5.2;
  0.6%; Score 20; DB
100.0%; Pred. No. 5.2
ive 0; Mismatches
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/product= Polymerase_I
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84. .1163
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 298. .2976
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ID XX07172
AC X07172
AC X07172
DT X07172
DT 21-MAY-1999 (first entry)
DE Soybean diaminopimelate epimerase; soybean Maminopimelate epimerase; soybean Maminopimelate epimerase; soybean Maminopimelate epimerase; soybean KW threonine; methionine; cysteine; KW crop improvement; food; feedstuff FH Key alycine max. Iocation/Qualifie: FH Key 84. .1163
FT W09855601-A2.
PD 10-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1136 catggaaccatggaggagga 1155
                                                                                                                                   17/c
Q23917 standard; DNA; 4286 BP.
Q23917;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       847 AATAATCTTTGAATTGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.6
Best Local Similarity 100.
Matches 20; Conservative
                                                        20; Conservative
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Q05640;
17-DEC-1990
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                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                       Syntherase

Claim 7: Page 41-42; 98pp; English.

This is the nucleotide sequence of a contig of cDNA clones

This is the nucleotide sequence of a contig of cDNA clones

Se2.pk0005:fl. ses8w.pk0010.hll. sfll.pk001.hls and sgslc.pk002.kl2

which codes for full-length soybean dlhydropicolinate reductase

(see W97731). The clones were isolated from soybean embryo (10

days after flowering), mature embryo (8 weeks after subculutre),

immature flower and seed (4 hr after germination) cDNA libraries

and identified by comparison to public sequence databases using

BLAST algorithms. The contig shows sequence similarity to the

Synechocystis sp. enzyme. The invention relates to new isolated

nucleic acid fragments (see X70166-85) encoding plant enzymes (see

W97727-44) that catalyse steps in the biosynthesis of lysine,

threonine, methodine, cysteine and isoleucine from aspartate, the

enzyme being selected from dihydropicolinate reductase,

claminopimelate epimerase, threonine synthase, threonine deaminase

cor S-adenosylmethionine synthetase. The invention also relates to

the construction of a chimeric gene encoding all or a portion of

the biosynthetic pathway enzyme in crop plants such as

corn, soybean and wheat can be used to alter levels of the amino

altered levels of the enzyme in a transformed host cells corn, soybean and wheat can be used to alter levels of the amino

acids in human food and animal feed. Transformed host cells corn, soybean and wheat can be used transformed host cells

Sequence 1301 BP; 333 A; 291 C; 313 G; 364 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The DNA sequence comprises a portion of a transposon INS-20 that affects expression and related cellular activity. The DNA has been reacted with advanced glycosylation end products and is typically in the form of an AGE plasmid that can be transfected into cells. The AGE modification of the plasmid may activate the transposons which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-1994 (first entry)
AGE-modified DNA INS-34.
Advanced glycosylation end products; AGE plasmids; transposon; ss.
MUS musculus.
WO9402599-A.
                                                                                                                                                                                                           New plant amino acid biosynthetic enzymes, DNA and chimeric genes encode: dihydropicolinate reductase; diaminopimelate epimerase; threonine synthase; threonine deaminase; S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Advanced glycosylation end-products, typically in the form of age-plasmids - can be transfected into cells and used to capture or activate transposons, e.g. to treat tumour cells Claim 6; Fig 3; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 19; DB 1; Length 1301;
100.0%; Pred. No. 16;
tive 0; Mismatches 0; Indels
                                                                         (DUPO) DU PONT DE NEMOURS & CO E I.
Abell LM, Allen SM, Falco SC, Hitz WD, Kinney AJ,
Rafalski JA, Thorpe CJ;
WPI; 99-070263/06.
P-PSDB; W97731.
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19-JUL-1993; U06754.

22-JUL-1992; US-920985.

UYRQ ) UNIV ROCKEFELLER.

Bucala RJ, Cerami A, Lee
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Matches 19; Conservative
                           12-JUN-1997; US-049443.
06-JUN-1997; US-048771.
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                                                                                                                                                                                                                                                                                               synthetase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pregnancy specific proteins, genes and antibodies - for use in dagnosis and in compsns. having immunosuppressive and growth promoting activities.

Claim 4; Fig 3; 78pp; English.

Claim 4; Fig 3; 78pp; English.

Mass is a clone encoding a placental pregnancy-specific protein (SPI) also known as pregnancy-specific beta glycoprotein (PSBG) which is detected in placenta and is membrane-bound. The sequence and Abs specific for it can be used in diagnosis, pregnancy testing and monitoring of tumours. The protein has immunosuppressive activity and growth promoting activity and can be used for enhancing fertility in females, viability of a foetus etc.
are captured. Such capture or movement of transposons in a cell be used to treat tumour cells. See also 057059-73. 464 A; 316 C; 353 G: 427 T:
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                                                                                                                          Length 1560;
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Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1990 (first entry)
Clone hPS2 encoding SP1-like protein.
Pregnancy-specific protein; carcinoembryonic antigen; CEA;
fertllity; abortion; placenta; ss.
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                                                                                                                                                                   0; Indels
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48;
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                                                                                                                                                                   Mismatches
                                                                                                                            Score 18;
Pred. No.
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1. 1065
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100.0%; Fre
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/*tag= d
/label= Rc
1705. .1710
/*tag= e
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286. .819
/*tag- b
286. .564
/*tag- c
/label- Rn
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                                                                                                                                               Local Similarity 100.
nes 18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JAN-1990; U00285.
18-JAN-1989; US-298638.
07-AUG-1989; US-390409.
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WPI; 90-253860/33.
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387 T;

640 G;

878 C;

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433 A;
   the extent of oxidisation. Sequence 2338 BP; 433
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Matches 18; Conserv
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                                         Sequence
                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Production of Sialic acids on carbohydrate(s) and the addition of Sialic acids on carbohydrate(s) and the acid addition of other members of the same gene family claim 6; Figure 20; 136pp; English.

Thuman Gal beta 1,3GalNAc alpha 2,3 Sialyltransferase is also called human ST30. In order to clone human ST30 sialyltransferase is called human ST30. In order to clone human ST30 sialyltransferase is conficient or human fetal brain total RNA was combined with each placenta or human fetal brain total RNA was combined with each contain the human ST30 sialylmotif as judged by homology with the portine sequence. A human placenta cDNA library was screened with the contain the human sT30 sialylmotif as judged by homology with the contain the human characterisation of the positive clones revealed cDNA of two types which differed in their 5' ends. The nt shown in Q8287.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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100.0%; Pred. No. 48;
tive 0; Mismatches 0; Indels
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14-NOV-1989; 005112.
14-NOV-1989; US-269669.
(GENZ-) Genzyme Corp.
Long S, Ostroff GR;
WPI: 90-193438/25.
PSDB; R05534.
Cloning vector contg. DNA from nocardioform microorganisms deoxyribonucleic acid.
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Recombinant cholesterol oxidase gene.
Cholesterol oxidase; pSL81; cholesterol; ds.
Rhodococcus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kelm S,
Wen X;
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146. .2026
/*tag= a
                                                                                                                                                                                                                                  Location/Qualifiers
931. .1953
/*tag= a
                                                                 Q82873;
27-SEP-1995 (first entry)
Human ST30 slalyltransferase.
Sialyltransferase; stalic acid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   27-JUL-1994; U08516.
04-AuG-1993; US-102385.
(REGC ) UNIV CALIFORNIA.
Burlingame AL, Gillespie W, Re
Medzihradszky K, Paulson JC, W
WPI: 95-090894/12.
                                     Q82873 standard; cDNA; 2070 BP
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19-0CT-1990
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Matches
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This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcr diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis.

Sequence 2341 BP; 1005 A; 238 C; 459 G; 639 T;
                                                                                                                                                                                                                                                                                                              31-MAR-1999 (first entry)
H. pylori GHPO 675 gene.
GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis; peptic ulcer disease; ss.
Helicobacter pylori.
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                                                    Gaps
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100.0%; Pred. No. 48;
Ive 0; Mismatches 0; Indels
  Length 2338
                                                    Indels
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29-UUL-1997; US-902615.
01-APR-1999; US-803457.
24-UUR-1997; US-881227.
(HUMA-) HUMAN GENOME SCI INC.
(INMR.) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Al-Garawi A, Rleanthous H, Miller C, Oomen RP, Tomb J; WPI; 98-54293446.
P-PSDB; W98274.
    DB 1;
                        red. No. 48;
Mismatches
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    0.6%; Score 18;
                             Pred. No
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100.0%; Pre
0;
100.08; Pre
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X13993;
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                           Best_Local Similarity 100.
Matches 18; Conservative
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Job time: 13534 sec
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Sequence Sequence

13, Appl 6, Appli 22, Appl 22, Appl 22, Appl 7, Appli 7, Appli

Sednence Sed

Appli Appli Appli Appli Appli

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US-0/-95/-434_11/C
| Sequence | 11, Application US/0797434 |
| Patent No. 5466591 |
| GENERAL INFORMATION: |
| APPLICANT: Gelfand, David H. |
| TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES |
| NUMBER OF SEQUENCES: 38 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Hoffmann-La Roche Inc. |
| STREET: 340 Kingsland Street |
| CITY: Nutley |
| STATE: New Jersey |
| COMPUTER: Readable FORM: |
| MEDIUM TYPE: Floppy disk |
| COMPUTER: Macintosh |
| COMPU
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US-08-970-740-137
US-08-677-012-6
US-08-677-012-6
US-08-477-728-96
US-08-477-728-96
US-08-477-000-96
US-08-477-000-96
US-08-477-000-96
US-08-477-000-96
US-08-640-389A-6
US-08-640-389A-6
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US-08-110-22
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US-08-002-324-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: 7
SOFTWARE: Wordberfect 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,394
FILING DATE: 15-MAX-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,394
FILING DATE: 12-JAW-1988
FILING DATE: 12-JAW-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 063,509
FILING DATE: 17-UGN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,241
FILING DATE: 22-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
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US-07-977-434-11/C
      ; Search time 124.08 Seconds (without alignments) 3615.164 Million cell updates/sec
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Sequence 11, Appl
Patent No. 5169835
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/cgn2_6/ptodata/2/lna/5B_COMB.seq:*
/cgn2_6/ptodata/2/lna/5C_COMB.seq:*
/cgn2_6/ptodata/2/lna/5D_COMB.seq:*
/cgn2_6/ptodata/2/lna/6_COMB.seq:*
/cgn2_6/ptodata/2/lna/FCOMB.seq:*
/cgn2_6/ptodata/2/lna/FCOMB.seq:*
/cgn2_6/ptodata/2/lna/FCOMB.seq:*
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-196-989B-1
US-08-36-1
US-08-35-267A-1
US-08-33-0621-19
PCT-US93-0621-19
US-08-299-849B-22
US-08-142-368A-22
US-08-142-368A-22
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US-08-627-254C-26
PCT-US95-13749-3
US-08-772-440-33
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-09-235-246-2
-08-889-909A-21
-08-724-774B-3
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US-08-458-819-11
PCT-US91-07035-11
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PCT-US91-02942-78
US-08-857-946-137
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-08-576-165-3
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    nucleic search, using sw model

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Gapop 60.0 , Gapext 60.0
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Match Length
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                                                                                                                                                                                                                  PRILING DATE: 28-5EP-1990
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 590,213
FILING DATE: 28-5EP-1990
PRIOR APPLICATION NUMBER: US 523,394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
FILING DATE: 12-JAN-1988
FILING DATE: 17-JAN-1988
FILING DATE: 17-JAN-1987
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 899,241
FILING DATE: 22-AUG-1987
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 899,241
FILING DATE: 15-AUG-1991
PRIOR APPLICATION NUMBER: US 585,471
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 585,471
FILING DATE: 22-DEC-1989
PRIOR APPLICATION NUMBER: US 609,157
FILING DATE: 22-DEC-1989
PRIOR APPLICATION NUMBER: US 609,157
FILING DATE: 24-JUL-1990
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 577,517
FILING DATE: 24-JUL-1990
PRIOR APPLICATION NUMBER: US 577,517
FILING DATE: ATUL-1990
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                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
                                        FILING DATE: 23-FEB-1993
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
      07/977,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: Cas
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2972
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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LENGTH: 2679 base pairs
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Best Local Similarity 100.
Matches 20; Conservative
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US-08-458-819-11
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APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 585,471

FILING DATE: 20-SEP-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 455,611

FILING DATE: 22-DEC-1989

PRIOR APPLICATION NUMBER: US 609,157

FILING DATE: 02-NOV-1990

PRIOR APPLICATION NUMBER: US 557,517

FILING DATE: 24-JUL-1990
ATPORNEY/AGENT INFORMATION:
FILING DATE: 24-JUL-1990
ATPORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,822

REFERENCE/DOCKET NUMBER: 31,822

RESTERNCE/DOCKET NUMBER: 31,822

RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFO
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US90/07641
FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20;
Pred. No.
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FILING DATE: 02-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-08-458-819-11/C
US-08-458-819-11/C
Sequence 11, Application US/08458819
Patent No. 5795762
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.6%; Sc
Best Local Similarity 100.0%; P.
Matches 20; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            550 AATAAICTIIGAAIIGIICI 531
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..2676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
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US-07-977-434-11
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APPLICANT: KLIS, FRANCISCUS M.
APPLICANT: SCHREUDER, MARRIEN P.
APPLICANT: TOSCHRA, HOLSER T.
APPLICANT: TOSCHRA, FROMELIS T.
TITLE OF INVENTION: CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION TITLE OF INVENTION: PROTEIN
TITLE OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New YORK AVENUE, N.W.
CITY: Washington
STATE: D. C.
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5169835-3/C
; Patent No. 5169835
APPLICANT: WAI-YEE, CHAN
TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
NUMBER OF SEQUENCES: 48
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/390,409
FILING DATE: 07-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%; Score 18; DB 7; Length 1693;
100.0%; Pred. No. 22;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                         0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,525
FILING DATE: 04-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                          0.6%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                                                                          ORGANISM: Thermosipho africanus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-362-525-21
Sequence 21, Application US/08362525
Patent No. 6027910
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.00,
100.0%; Pre-
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                DNA (genomic)
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Best Local Similarity 100.0
Matches 20; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
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linear
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              MOLECULE TYPE: DN HYPOTHETICAL: NO
                                                ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 1693
5169835-3
                                                                                                                                 ; LOCATION:
PCT-US91-07035-11
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APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
TITLE OF INVENTION: G-Frotein Coupled Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          0; Indels
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ZIP: 32606
ZUP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,936
FILLING DATE: December 6, 1996
CLASSIFICATION: 536
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22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 3; Pred. No. 22; 0; Mismatches
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Pred. No.
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NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MAC-100C1
TELECOMMUNICATION: 1NFORMATION:
TELEPHONE: 352-375-8100
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100.0%; Pi
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; Patent No. 5856443
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Best Local Similarity 100.0%; P.
Matches 18; Conservative 0;
               TELECOMMUNICATION INFORMATION:
                            TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2754 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-196-989B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-760-936-1
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INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 100.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
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; OTHER INFORMATION: /product- "Flocculation protein" /gene- nFLO1"
US-08-362-525-21
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100.0%; Pred. No. 22;
ive 0; Mismatches 0; Indels
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,989B
                                       AFLICATION NOBER: EF 9220280.3

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92203899.7

FILING DATE: 14-DEC-1992

PRIOR APPLICATION NUMBER: EP 1203899.7

PRIOR APPLICATION NUMBER: PCT/EP93/01763

ATORNEY/AGENT INFORMATION:
NAME: ROUGHIS, PADL N.
RECISTRATION NUMBER: 213289/T7020(V)

TELEPHONE: (202) 861-3000

TELEFAX: 6714627 COSH

INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
LENGTH: 2685 Dase pairs

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
IMMEDIATE SOURCE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92202080.5
FILING DATE: 08-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
ATTORNEY_AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MAC-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08; PAY
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Best Local Similarity 100.
Matches 18; Conservative
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RESULT 10
PCT-US93-06251-19
PCT-US93-06251-19
FGENERAL INFORMATION:
FGENERAL INFORMATION:
FGENERAL INFORMATION:
FITLE OF INVENTION:
FITLE OF INVENTION:
FITLE OF INVENTION:
FITLE OF INVENTION:
FORRESPONDENCE ADDRESS:
FORRES
                                                                       APPLICANT: Calabretta, Bruno
APPLICANT: Calabretta, Bruno
APPLICANT: SKORSKI, TOMASZ
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENE ADDRESS: 55
CONTRESSEE: Seddel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDLING TYPE: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US93/06251
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OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MODICO, DATIEL A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 568-539
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pr
ative 0;
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nucleic acid
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Best Local Similarity 100.(
Matches 18; Conservative
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                                            GENERAL INFORMATION:
APPLICANT: Calabr
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Sequence 1, Application US/08325267A

Sequence 1, Application US/08325267A

Sequence 1, Application US/08325267A

Sequence 1, Application US/08325267A

SERICANT NOTATION:

APPLICANT: TAKATA, YOSHIHIRO

APPLICANT: ONNELA, MAIJA-LEENA

APPLICANT: NENTILA, MAIJA-LEENA

APPLICANT: RERANEN, SIRKKA

TITLE OF INVENTION: CONTAINING THEM

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSE: ADDRESSE: ADDRESS:

ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

STARET: 1755 S. JEFFERSON DAVIS HWK, SUITE 400

CITY: ARLINGTON

STARET: VA
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OURTHAND SYSTEM:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/325,267A
FILING DATE: 18-NOV-1994
CLASSIFICATION NUMBER: US/08/325,267A
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/1/1993
FILING DATE: 24-FEB-1994
PRIOR APPLICATION NUMBER: 24,618
FILING DATE: 26-FEB-1993
ATTONNEY/AGENT INPORMATION:

NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION STATE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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STRAIN: ABXL-1D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA

ITE: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 ctgtgattgttatcagaa 106
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; LOCATION: 1..4
US-08-325-267A-1
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; Sequence 19, Application US/08306691B; Patent No. 5734039

US-08-306-691B-19

2948 CIGIGALIGITALCAGAA 2965

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ATTORNEY/AGENT INFORMATION:
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US-08-29-849B-22/C
; Sequence 22, Application US/08299849B
; Patent No. 5612201
; GENERAL INFORMATION:
    APPLICANT: De Plaen, Etlenne; Boon-Falleur, Thierry;
    APPLICANT: Chomez, Patrick
    TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
    TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
    NUMBER OF SEQUENCES: 48
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Felife & Lynch
    STREET: 805 Third Avenue
    CITY: New York City
    STATE: New York
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21;
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER LIBM COMPUTER: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM COMPUTER: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM COMPUTER: IBM COMPUTER: COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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100.0%; Pred. No.
tive 0; Mismatc
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FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
                         CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Didigilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 34227 TGCTGCAGCCCAACAACT 34244
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Best Local Similarity 100.0
Matches 18; Conservative
FILING DATE: 19930630
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NAME: BEAGO, NO. 551201man D.
RECEIGNATION NUMBER: 30,946
RECEIGNATION PROPERTION STATEMENT OF STATEMENT OF
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Patent No. 5821091
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                             Length 920
                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
5510472-1
;PATENT NO. 5510472
APPLICANT: REVEL, MICHEL;TIOLLAIS, PIERRE
; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT HUMAN
                                                                                                                                                                                                                                                                                                                                DB 5;
. 67;
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:

PELLICATION NUMBER: US/07/883,633

FILING DATE: 15-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 208,925

FILING DATE: 12-DEC-1980

APPLICATION NUMBER: 860,883

FILING DATE: 12-DEC-1986

APPLICATION NUMBER: 208,925

FILING DATE: 20-NOV-1986

FILING DATE: 20-NOV-1980
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100.0%; Pre
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Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
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IBM PC compatible
                                                  LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2277 acagccaggggagcctg 2293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 ACAGCCAGGGGAGCCTG 418
                                                                                                                                                                                                                     ; NAME/KEY: MAGE-10 gene
US-08-967-727-22
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 17; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 350 Cam
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US-08-592-126-97
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APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;

APPLICANT: Van der Bruggen, Pierre; Boon-Falleur, Thierry

TILE OF INVENTION: Tand Rejection Antigen Precursor Mage-3 And Uses Thereof

TILE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: New York City

STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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67:
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STREET: 805 TILL.
CITY: New YORK City
STATE: New YORK
ZIP: 10022
COMPUTER READABLE FORM:
MEDIOM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: EDSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,727
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: OFT/US92/04354
FILING DATE: 22-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/08967727 Patent No. 6025474
  TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2277 acagccaggggagcctg 2293
                         TELEPHONE: (212) 688-920
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 ACAGCCAGGGGAGCCTG 418
                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                    ; NAME/KEY: MAGE-10 gene
US-08-142-368A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-08-967-727-22/c
                                                                                                                                                                                                                                                                              FEATURE
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Ouery Match 0.5%; Score 17; DB 2; Length 1534; Best Local Similarity 100.0%; Pred. No. 67; Matches 17; Conservative 0; Mismatches 0; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
FILING DATE:
CLASSIFICATION: 435
ATTONEX/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 1534 base pairs
TYPORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 1534 base pairs
TYPOLLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHERICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Septin-2.seq
US-08-592-126-97
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0; Gaps

Search completed: September 3, 2000, 17:49:21 Job time: 17200 sec

us-09-183-972-3_1.rst

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9b_est25;
9b_est28;
9b_est28;
9b_est28;
9b_est28;
9b_est28;
9b_est28;
9b_est31;
9b_est31;
9b_est31;
9b_est32;
9b_est34;
9b_est34;
9b_est43;
9b_est43;
9b_est43;
9b_est43;
9b_est43;
9b_est43;
9b_est44;
9b_est
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9D_est48**.*
9D_est51.**
9D_est52.**
9D_est52.**
9D_est53.**
9D_9ss1.**
9D_9ss1.**
9D_9ss2.**
em_gss1.**
em_gss1.**
em_gss2.**
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gb_gss5:*
gb_gss6:*
gb_gss7:*
gb_gss8:*
em_gss9:*
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em_gss7:*
em_gss8:*
em_gss9:*
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gb_gss11:
em_gss12:
gb_gss12:
; Search time 2738.16 Seconds
(without alignments)
5251.866 Million cell updates/sec
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                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                             3, 2000, 10:24:07
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                           US-09-183-972-3
3261
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em_est2::*
em_est3::*
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em_est5::*
em_est6::*
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em_est10::*
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Maximum DB seq length: 1000000
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9b_est16:
9b_est17:
9b_est18:
9b_est20:
9b_est21:
9b_est21:
9b_est23:
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                                                                                                                                                                                                                                                       Title:
Perfect score:
Sequence:
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9b_9ss13:*
9b_9ss14:*
9b_9ss15:*
9b_9ss16:*
9b_9ss17:*
9b_9ss18:*
em_9ss13:*
117:
118:
119:
120:
121:
123:
123:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## W26960 16610 Human H38604 yp48e04.rl AA226663 EST30113 H38594 yp48e04.rl AA23618 EST30113 H38594 yp48e06.rl AL10613 mp95s12.r AL116463 mp95s12.r AL030162 Fugu rubr AC030162 Fugu rubr AC030163 Prosophil AL06195 Drosophil AL06195 Drosophil AL060192 Drosophil AL060192 Drosophil AL060193 Drosophil AL06196 Drosophil AL06196 Drosophil AL069106 Drosophil AL069106 Drosophil AL069106 Drosophil AL069106 Drosophil AL069106 Drosophil AL069106 Drosophil AL069109 Brosophil Description W26960 H23664 H23664 H236663 H236663 H236268 H259278 H25927 SUMMARIES DB Length % Query Match Result No. O

## ALIGNMENTS

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RESULT 1 W26960/c					
LOCUS	W26960	561 bp	mRNA	EST 08-MAY-1996	
DEFINITION	16h10 Human	retina cDNA	randomly primed	DEFINITION 16h10 Human retina cDNA randomly primed sublibrary Homo sapiens	S
	CDNA, mRNA sequence.	seguence.			

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Query Match
Best Local Similarity 99.0%;
Matches 377; Conservative
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AA326863
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The Washd-Merck EST Project

Unpublished (1995)

On May 1998 this sequence version replaced gi:3138652.

Contact: Wilson RK
Washington University School of Medicine
(4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Fax: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukarrota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 405)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
1518 ccacagatacaatggccactgaccagacaatgctagtaccagggctcaccatccccacca 1577
                                                                                                             173 CCACAGANACAATGGCCACTGACCAGACAATGCTAGTACCAGGGCTCACCATCCCCACCA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                  H38604 405 bp mRNA EST 16-AUG-1995
ypd8604.rl Soares retina N2b4HR Homo saplens CDNA clone
IMAGE:190686 5', mRNA sequence.
H38604
H38604.1 GI:908103
                                                                                                                                                                                                                                 1638 atgacagccgatcaagtg-caggtggcgaagatatggtcagacaccta 1684
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/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                          53 ATGACAGNCGATCAAGTGAGAGGTGGCGAATAAATGGCGNGNCCCANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:3847095"
/db_xref="taxon:9606"
/clone="InAGE:190686"
/clone=lib="Soares retina N2b4HR"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .405
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H38604
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95

BASE COUNT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 32)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earl-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., Kobondid, L.A., Nguyen, D.T., Pelligrin, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Watdman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrley, R., Fischer, C., Hastnags, G.A., Kozak, D.L., Kunsch, C., Hunglun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Fraser, C.M., and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nuclectides of cDNA sequence
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end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                               121 CTTGAGACAGTGGACGGAGCAGAGCATGGTCTACCTGACACTTCTTGGTCTCCACCTGCT 180
                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAAATTGCTGGATCACTGCCAGCCTTTGGTCCTGACACCCAATCAGAGCTGCCCACATCT
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     Length 405;
                                                       Indels
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EST30113 Cerebellum II Homo sapiens cDNA 5'
AA326863 GI:1979130
Score 354.4; DB 85;
Pred. No. 2.3e-81;
0; Mismatches 2;
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Seg primer: M13RP1
High quality sequence stop: 106.
Location/Qualifiers
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Emax: 3018699423
Emax: 3018699423
For clone availability, additional sequence and expression
for clone availability additional sequence and expression availability ad
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1 (bases 1 to 309)

11 (lark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="cerebellum"
/dev_stage="adult"
/note="Organ: brain; Vector: pBluescript SK-; Site_1:
Ecomi; Site_2: xho!" 85 t 5 others
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YP48c06.rl Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:190666 5', mRNA sequence.
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On May 18, 1998 this sequence version replaced g1:3138642.
Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.7%; Score 317; DB 24; Length 322;
ilarity 98.4%; Pred. No. 1.1e-71;
Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                              /db_xref="ATCC (inhost):127542"
/db_xref="taxon:9606"
/clone_lib="Cerebellum II"
                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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H38594.1 GI:908093
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Matches 317; Conserv
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JOURNAL
COMMENT
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AUTHORS
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/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DHIDB (amptcillin resistant)"
/lab_host="DHIDB (amptcillin resistant)
/lab_host="DHIDB (amptcilling re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
Insert Size: 2489
High quality sequence stops: 106
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@mage.llnl.gov) for further information.
Insert Length: 2489 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-1997
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Pred. No. 5.8e-67;
0; Mismatches 6; Indels
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:3847075"
/db_xref="taxon:9606"
/clone="InAGE:190666"
/clone=lib="Soares retina N2b4HR"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
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namumatia: Eutcilia; FILMmates; Catarrinii; Hominidae; Homo.

I (bases 1 to 298)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.G., Man-Wail, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Giehm, C.L., Hanna, M.C., Hedblon, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Lulu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Fyder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hastings, G.A.,
Raymond, L., Weil, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
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10.298

Application/Qualifiers

10.298

Application of the control of the c
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Email: arkerlavetigr.org
information and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
EST10795 Umbilical vein endothelial cells II Homo sapiens cDNA 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2731 cccaaatgcaatcagcgaaacatatttttactattcttggatgatagtcaaaatgatcat 2790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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The Institute for Genomic Research
The Institute for Genomic Research
The MD 20850 USA
Tel: 3018699056
Fax: 3018699423
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99.3%; Pred. No. 6.1e-65;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
                                                                                                                              AA296278.1 GI:1948653
                                              end, mRNA sequence.
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                                                                               AA296278
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Tumor Gene Index
Unpublished (1997)
On May 18, 1998 this sequence version replaced gi:3136559.
On May 18, 1998 this sequence version replaced gi:3136559.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert-Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the correct orientation)
Seq primer: -40RP from Gibco.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bumanlai; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 481)
NCI-GGAP http://www.ncbi.nlm.nfh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2226 taaagaacgaacggactgaggaagcggagtgtcgctgcaaaccaggatatgacagccagg 2285
62 AACCAGCTGATCAGGCGGATCCCTGCAAACTCCTAGACTGTGGCAAATTTGCCCAGTGTG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                   Length 481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:1000"
/clone="IMAGE:577006"
/clone_lib="Soares_thymus_2NbMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4" weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.2%; Score 200.8; DB 40; Similarity 71.7%; Pred. No. 2e-41; 77; Conservative 0; Mismatches 112;
                                                                                                                                                                                                                                    AI510373
AI510373.1 GI:4409278
                                                                                                                                                                                                                                                                                           house mouse.
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Best Local Simi
Matches 307;
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
                                                                                                                                                                                                    DEFINITION
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TITLE
                                                                                                                                                             AI510373
LOCUS
                                                                                                                                                                                                                                        ACCESSION
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AL030162
AL030162.1 GI:3272276
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                                                                                                                                                                                                                                                                                                                                                                                                                                AA116463 495 bp mRNA EST 17-FEB-1997
mp95e12.rl Soares_thymus_2NDMT Mus musculus cDNA clone IMAGE:577006
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fmail: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:351654
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Unpublished (1996)
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/db_xref="taxon:10090"
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/lab_host="DH10B"
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and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatlan Bonaldo."
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[ (bases 1 to 600)
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Vector: pBluescript II KS
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Williams,G. and Brenner,S.
Direct Submission
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Fugu rubripes GSS sequence, clone 184G17ab12, genomic survey
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Length 647;

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District Control of the Canadata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 830)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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/db_xref="taxon:9606"
/clone="Plate=2046 Col=5 Row=P"
/clone="Lib="CIT Approved Human Genomic Sperm Library D"
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                                        Similarity 100.0%; Score 81; DB 95; Length 64 Similarity 100.0%; Pred. No. 2.9e-10; 11; Conservative 0; Mismatches 0; Indels
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11arity 89.5%; Pred. No. 1e-09;
Conservative 0; Mismatches 10
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 647)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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/db_xref="taxon:9606"
/clone="Plate=2057 Col=9 Row=A"
/clone=!b="CIT Approved Human Genomic Sperm Library D"
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HS_2057_Al_AO5_MR CIT Approved Human Genomic Sperm Library D
Homo sapiens genomic clone Plate=2057 Col=9 Row=A, genomic
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                                                                                                                                                              Query Match 2.8%; Score 90.6; DB 122; Length 600; Best Local Similarity 67.6%; Pred. No. 9.1e-13; Matches 123; Conservative 0; Mismatches 59; Indels 0;
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Fax: (206) 616-3887
Fax: (207) For Sequence Tagged Connector
Plate: 2057 Fow: A column: 9
Class: BAC ends
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/organism="Fugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid 184G17"
/clone="144G17ab12"
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVYR cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Razuctoyo Ososegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
ECORI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
Pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                        Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR31021 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Genoscope.
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/db_xref-"taxon:7227"
/clone_lib-"RPCI-98"
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Direct Submission

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

Petermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley brosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecori digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the Same strain used for the BDGP's pl and BSI libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://warnar.med hu.ffalo.edu/Afrosophila har htm.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                      tagtcaaaaatgatcataagccaggtttgcttccaccttccctgaaaattttactcacaga
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Matches 115; Conservative
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                                                    121 agccagaatgtatttggaaactagaagactattttttgttttttggattttctccaagt 180
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Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y., Williams,G. and Brenner,S.
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Fugu rubripes GSS sequence, clone 184G17aE12, genomic survey
sequence.
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/organism="Fugu rubripes"
/db_xref="taxon:31033"
/clone_llb="cosmid 184617"
/clone="184617aE12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-JUN-1998) MRC H. Centre, Hinxton, Cambridge, Cl blobelp@hgmp.mrc.ac.uk
V-type: phagemid
PRIMER: KS
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GSS; genome survey sequence.
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Principle of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org the BDGP Drosophila melanogaster BAC ibrary was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR35M04 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL073856
AL073856.1 GI:4953838
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
Genoscope.
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Determination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a thirp.//www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                    CNSO161H 1201 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15018 of DrosBAC library from Drosophila melanogaster (fruit
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/plasmid="pselobAcil"
/db_xref="taxon:7227"
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Searched:

Run on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	AF047491 Macaca fa	AF047492 Homo sapi	2 Ното	AL157379 Homo sapi	1 Homo	5 Homo	9 Ното	AF017763 Homo sapi	AF017766 Homo sapi	AF017764 Homo sapi	7 Homo	AC017079 Homo sapi	AC009837 Homo sapi	AC031980 Homo sapi	297054 Human DNA s	AL109851 Homo sapi	AF106667 Mus muscu	AC021257 Homo sapi	AC061964 Homo sapi	AL109805 Human DNA	AF222684 Homo sapi	AC004692 Homo sapi	AC021544 Homo sapi	AP001811 Homo sapi
SUMMARIES		DB ID	1 1 ANERX STAIGH	39 AF047492	11 HSIMPG03	32 AL157379	11 HSIMPG02	11 HSIMPG06	32 AL157379	11 HSIMPG04	11 HSIMPG07	11 HSIMPG05		55 AC017079		72 AC031980	-	32 HS1036D20	13 AF106667	-	78 AC061964	11 HSDJ581P3	39 AF222684	39 AC004692	74 AC021544	31 AP001811
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	& Query	Match	100.0	20.2	15.3	15.3	7.7	7.4	7.4	5.4	4.3	4.1	4.0	4.0	3.8	3.8	3.6	3.6	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4
		Score	555	112	85	85	43	41	41	30	24	23	22	22	21	21	20	20	19	19	19	19	19	19	19	19
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19 3.4 158230 56 AC012134 AC012134 Homo sapt 19 3.4 155946 73 AC012571 AC024711 Homo sapt 19 3.4 151594 68 AC024711 AC005304 Homo sapt 19 3.4 151591 68 AC025526 Homo sapt 19 3.4 156772 68 AC025526 Homo sapt 19 3.4 15772 58 AC02451 Homo sapt 19 3.4 15772 51 AP001158 Homo sapt 19 3.4 170398 32 CNS01DTH AL132719 Homo sapt 19 3.4 176126 31 AP000762 Homo sapt 19 3.4 17614 68 AC025413 AC02542 Homo sapt 19 3.4 201744 80 AC02543 AC02348 Homo sapt 19 3.4 201744 80 AC055758 Homo sapt 19 3.4 201741 31 AP001159 Homo sapt AC05575 Homo sapt 19 3.4 201741 31 AP001321 AC05758 Homo sapt 19 3.4 212411 31 AP001321 GG31948 Homo sapt AP001321 Homo sapt 3.2 21315 31 AB001321 Homo sapt AP001321 Homo sapt AP001321 Homo sapt 3.2 21313 AP001321 Homo sapt AP001321 Homo sapt AP001321 Homo sapt 3.2 21313 AP001321 Homo sapt AP001321 Homo sapt 3.2 21313 AP001321 Homo sapt AP001321 Homo sapt 3.2 21313 AP0	AF047491 555 bp mRNA PRI 24-FEB-1998 /O2(a) Nacaca fascicularis interphotoreceptor matrix proteoglycan 150 mRNA, partial cds. NAF047491.1 GI:2906229 Crab-eating macaque. Macaca fascicularis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Macaca Eucheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;			EEGXVELSISLINGREKAELADSOS*  162 a 131 c 131 g 131 t  tch 100.0%; Score 555; DB 11; Length 555; al Similarity 100.0%; Pred. No. 0; 555; Conservative 0; Mismatches 0; Indels 0;
0 00 00 00 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 AC047491 AC0CUS DEFINITION ACCESSION VERSION VERYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOURC	BASE COUNT ORIGIN Query Match Best Local S Matches 555

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Sims,S.
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/protein_id="MAC03789.2"
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REFPRRKDEISAERTLGEPETIVISTOVANVSLGFPFLTPDDTLLNFILDNTLNDTK
RPTTERFERAVLEEORYELSVSLYNOKFKAELADSOSYYGELAGKSOLOMOKIFKK
LPGFRKIHVLGFREKKENGSSSTEWQLTATFKRHSARAKSPASDLLSFDSNKIESEE
VYHGTWEEDKQPRIYLTBDATLSFREKTISKALEEEQSLDVGTIQFTDEIAGSLPAFGDDTG
SELPTSFAVITEDATLSFREKTISKALEEEQSLDVGTIQFTDEIAGSLPAFGDDTG
SELPTSFAVITEDATLSFREKTISKALEEEQSLDVGTIQFTDEIAGSLPAFGDDTG
SELPTSFAVITEDATLSFREEDFYLDTWATDGATLDTWATDGATLDTGSSDDSRS
FMASSIFSLTDQGTTDTMATDQTMLVPGLITPTSDYSAISQLALGISHPPASSDDSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAGGEDMYRHLDEMDLSDTPARSEVPELSEYYSVPDHFLEDTTPYSALQYITTSSMTI
APKGRELYVPFSLRVANMAFSNDLFNKSSLEYRALEQOFTQLLVPYLRSNLTGFKQLE
DADPRESTYTVNSKKFAKSYPYNLTKAVHGYLEDFRSAAAQQLALETDSYSLNIEPA
DQADPCKFLYGGEFAQCYKNERTEEAECRCKPGYDSGGSLDGLEPGLGGPGTKECEVL
QGKGAPCRLPDHSENAXKTSYKFONQQNNKVISKRNSELLTVEYEEFNHQDWEGN"
724 c 664 g 836 t
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Gehrigh,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.E.
and Weber,B.H.F.
Assessment of a novel interphotoreceptor matrix gene (IPM150)
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Homo sapiens interphotoreceptor matrix gene (IPM150), exon 3.
AF017762.1 GI:3800717
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1 (bases 1 to 422)
Felbor, U., Gehrig, A., Sauer, C.G., Marquardt, A., Kohler, M., Schmid, M. and Weber, B.H.
Genomic organization and chromosomal localization of the
Sequence update by submitter
On Oct 26, 1999 this sequence version replaced gi:2906231.
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                                Location/Qualifiers

1. 3268
/organism-"Homo sapiens"
/db.xref-"taxon:9606"
/chromosome="6"
/map-"between markers D6S280 and D6S1659"
/ilssue/ppe="retina"
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                                                                                                                                                                                                                  /gene="IMPG1"
131. .2524
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/note="IPM 150"
                                                                                                                                                                                                                                                                                                                 /codon_start=1
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Dinassion
Submitted (22-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire,
Callo 18A, UK. Famaile nequiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Mar 6, 2000 this sequence version replaced gi:7009540.
IMPORRANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in
progress and the release of this data is based on the understanding
that the sequence may change as work continues. The sequence may
be contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
contig_ID: 00151 Length: 8447bp
Contig_ID: 00155 Length: 8443bp
Contig_ID: 0037 Length: 5047bp
Contig_ID: 0037 Length: 5047bp
Contig_ID: 0037 Length: 1155bp
Contig_ID: 00414 Length: 15535bp
Contig_ID: 00414 Length: 15535bp
Contig_ID: 00414 Length: 15535bp
Contig_ID: 00598 Length: 1028bp
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Contig_ID: 00598 Length: 6841bp
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 194704)
localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PDCRA), and North Carolina macular dystrophy (MCDRI) (Unpublished 3 (bases 1 to 422) (Belbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F. Direct Submission Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany
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15.3%; Score 85; DB 11; I
Best Local Similarity 100.0%; Pred. No. 4.2e-37;
Matches 85; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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112. .278
/gene="IPM150"
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contig_ID: 00/00 Length: 1115bp
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Contig_ID: 00925 Length: 2481bp
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Contig_ID: 01120 Length: 2716bp
Contig_ID: 01180 Length: 179bp
Contig_ID: 01186 Length: 179bp
Contig_ID: 01186 Length: 179bp
Contig_ID: 01370 Length: 1498bp.
* NOTE: This is a 'working draft' sequence. It currently
consists of 28 contigs. The true order of the pieces
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the axact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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7418 15864: contig of 8447 bp in length
15865 16664: gap of 800 bp
16665 18537: contig of 1873 bp in length
1658 19337: gap of 800 bp
19338 26186: contig of 6849 bp in length
26187 26986: gap of 800 bp
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f 1165 bp in length
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 537)

1 (bases 1 to 537)

2 (chases 1 to 537)

3 (chases 1 to 537)

4 (chases 1 to 537)

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Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. and Weber, B.H.F.
and Weber, B.H.F.
Assessment of a novel interphotoreceptor matrix gene (IPMI50)
localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI)
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Homo sapiens interphotoreceptor matrix gene (IPM150), exon 2.
AF017761
AF017761.1 GI:3800716
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Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
Direct Submission
189967 190766: gap of 800 bp
190767 192406: contig of 1640 bp in length
192407 193206: gap of 800 bp
193207 194704: contig of 1498 bp in length.
Location/Qualifiers
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100.0%; Pred. No. 3.4e-37;
11ve 0; Mismatches 0;
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    11. .194704
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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/clone_lib="RPCI-1"
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/gene="IPM150"
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85; Conservative
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Use Submission

Locate Submission

Locating 1.2.

Submitted (22-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire, Cabbo 158, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Mar 6, 2000 this sequence version replaced gi:7009540.

IMPORTARY: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate contig_ID: 00126_Length: 84.7bp

Contig_ID: 00126_Length: 84.7bp

Contig_ID: 00275_Length: 64.9bp

Contig_ID: 00377_Length: 3565bp

Contig_ID: 00377_Length: 3565bp

Contig_ID: 00377_Length: 1124bp

Contig_ID: 00377_Length: 1124bp

Contig_ID: 00377_Length: 11262bp
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contig_ID: 00934 Length: 10010bp

Contig_ID: 01026 Length: 2716bp

Contig_ID: 01069 Length: 2283bp

Contig_ID: 01121 Length: 2031bp

Contig_ID: 01186 Length: 1779bp

Contig_ID: 01186 Length: 1779bp

Contig_ID: 01386 Length: 1779bp

Contig_ID: 01386 Length: 1478bp

Contig_ID: 01386 Length: 1478bp

Contig_ID: 01386 Length: 1478bp

Contig_ID: 01386 Length: 1498bp.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 28 contigs. The true order of the pieces

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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                                                                        REFERENCE
AUTHORS
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Gehrig,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.E. and Weber,B.H.F.
Assessment of a novel interphotoreceptor matrix gene (IPM150)
localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI)
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Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
Direct Submission
Submitted (09-400-1997) Humangenetik, Universitaet Wuerzburg, Am
Hubland, Wuerzburg D-97074, Germany
Location/Qualifiers
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                HSIMPG06 311 bp DNA PRI 28-OCT-1998
Homo sapiens interphotoreceptor matrix gene (IPM150), exon 6.
AF017765
AF017765.1 GI:3800720
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 311)
Felbor, U., Gehriga,, Sauer, C.G., Marquardt, A., Kohler, M.,
Schmid, M. and Weber, B.H.
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Homo sapiens chromosome 6 clone RP1-62L18, *** SEQUENCING IN
PROGRESS ***, 28 unordered pieces.
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      Length 537;
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ilarity 100.0%; Pred. No. 3.6
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/db_xref="taxon:9606"
/chromosome="6"
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/gene="IPM150"
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Chases 1 to 377)

Gehrig,A., Meumenee-Hussels,I.E.

Gehrig,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.E.

Assessment of a novel interphotoreceptor matrix gene (IPM150)

localized to 6q14.2-q15 in autosomal dominant Stargardt-like

macular dystrophy, progressive bifocal chorioretinal atrophy

(PBCRA), and North Carolina macular dystrophy (McDRI)
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for 6q-linked retinopathies
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
            (bases 1 to 300)
rig,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.E.
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Onpublished

Onpublished

Relbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.

Direct Submission

Submitted (09-Aug-1997) Humangenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany

Location/Qualifiers
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Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
Direct Submission
Submitted (09-Ad0-1997) Humangenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany
Location/Qualifiers
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Homo saplens interphotoreceptor matrix gene (IPM150), exon 7.
AF017766
                                  Gehrig, A., Felbor, U., Kelsell, R., Hunt, D. M., Maumenee-Hussels, and Weber, B.H.F.
Assessment of a novel interphotoreceptor matrix gene (IPMISO) localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI)
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1 (bases 1 to 377)
Felbor, U., Gehrig, A., Sauer, C.G., Marquardt, A., Kohler, M., Schmid, M., and Weber, B.H.
Genomic organization and chromosomal localization of the
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Matches 30; Conservative 0; Mismatches 0;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 300)
Felbor, U., Gehrig, A., Sauer, C.G., Marquardt, A., Kohler, M., Schmid, M. and Weber, B.H.
Genomic Organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate for Gq-1inked retinopathies
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Homo saplens interphotoreceptor matrix gene (IPM150), exon 4.
AF017763
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81904 82931: contig of 1028 bp in length 82932 83731: gap of 800 bp 81332 91019: contig of 7288 bp in length 91020 91819: gap of 800 bp 91820 91860: contig of 6841 bp in length 91820 91860: contig of 6841 bp in length 100576: lo1375: gap of 800 bp 101376: lo1375: gap of 800 bp 11439 114318: contig of 113763 bp in length 11439 114318: contig of 12763 bp in length 11439 11842: contig of 23204 bp in length 118943 138442: contig of 800 bp 138943 138442: contig of 800 bp 14724 147223: contig of 800 bp 14724 14723: gap of 800 bp 15429 15428: gap of 800 bp 15429 15428: contig of 6805 bp in length 15429 155288: contig of 100 bp 156289 157088: contig of 100 bp 167089 167089: contig of 2316 bp in length 16709 167089: contig of 2316 bp in length 16709 167089: contig of 2316 bp in length 16709 167089: contig of 2316 bp in length 173698 174497: gap of 800 bp 17441: 173698 174497: gap of 800 bp 17441: 173698 174497: gap of 800 bp 17441: 173698 174497: gap of 800 bp 174418 17458 174598 174497: gap of 800 bp 174418 17458 174547: gap of 800 bp 174418 17458 174547: gap of 800 bp 174418 17458 174547: gap of 800 bp 174418 17458 174497: gap of 800 bp 174418 17458 174497: gap of 800 bp 174418 174597: contig of 2583 bp in length 174489 174418 174548 174489 174418 174548 174418 174548 174489 174418 174548 174489 174418 174548 174489 174489 174497: gap of 800 bp 1744497: gap of 800 bp 1744497: gap of 800 bp 1744497: gap of 800 bp 1744497 174489 174489 1744497: gap of 800 bp 1744497 174489 1744497 174489 1744497 174489 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 174491 17
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutherson, R.H.

The sequence of Homo sapiens clone

In published

L. Obases 1 to 170439)

Waterston, R.H.

Direct Submission

University School of Medicine, 4444 Forest Park Parkway, St. Louis, Mo 63108, USA

MO 63108, USA

ON NOV 9, 1999 this sequence version replaced gi:6249750.

* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. The true order of the places

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will

* be preserved.
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AC017079/c
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AUTHORS
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JOURNAL
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1 (bases 1 to 304)
Felbor, U., Gehrig, A., Sauer, C.G., Marquardt, A., Rohler, M., Schmid, M. and Weber, B.H. Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate for Gq-linked retinopathies
Gytogenet. Cell Genet. 81 (1), 12-17 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 304)
Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. and Weber, B.H.F.
Assessment of a novel interphotoreceptor matrix gene (IPM150)
localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDR1)
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Homo sapiens clone NH0480N09, WORKING DRAFT SEQUENCE, 1 unordered
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(Dases 1 to 304)

Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.

Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.

Blirect Submission

Submitted (Merzburg D-97074, Germany

Hubland, Wuerzburg D-97074, Germany
                                                                                                                                                                                                                                                                                                                        HSIMPG05 304 bp DNA PRI 28-OCT-1998
Homo sapiens interphotoreceptor matrix gene (IPM150), exon 5.
AF017764
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/db_xref="taxon:9606"
/chromosome="6"
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107. .171
                                                                                                                                                                                                                          190 GAGGAGCAGAGGTGGAGCTCAGC 213
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                  /gene="IPM150"
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HSIMPG05
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270 others

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T (bases I to 183375)
Waterston,R.H.
Direct Submission
Submitted (09-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Mar 7, 2000 this sequence version replaced 91:6554070.
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                                                                                                                                                                                                                                                                                                                   AC017079 183375 bp DNA HTG 07-MAR-2000
Homo sapiens chromosome 2 clone RP11-462M9, WORKING DRAFT SEQUENCE,
11 unordered pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                 Gaps
                                                              ö
Query Match 4.0%; Score 22; DB 42; Length 170439; Best Local Similarity 100.0%; Pred. No. 0.28; Matches 22; Conservative 0; Mismatches 0; Indels 0;
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Center code: WUGSC
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Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                    AC017079.2 GI:7193118
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                 Db 17640 CAGGACTGGGTCAGCTTCTGCC 17619
                                                                                                                      157 caggactgggtcagcttctgcc 178
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Shares to 164180)

Shares to 164180)

Shares to 164180)

Sharen B., Linton, L., Banna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangalo, M., Collins, S., Collymore, A., Castle, A., Cerny, J., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Funke, R., Gage, D., Galagan, J., Howland, J.C., Jones, C., Kann, L., Raratas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McEwan, P., McEwan, P., McEwan, P., McEwan, P., McEwan, P., McHandin, J., Marjor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavillin, B., Peterson, K., Pollara, V., Kiley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stołanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wux, Wyman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_wallsions@genome.wi.mit.edu
center project Information
Center clone name: 1804
Center clone name: 1804
Center clone name: 1804
Center clone name: 1804
Sequencing vector: M13; M77815; 968 of reads
Sequencing vector: M13; M77815; 968 of reads
3.82372002592353Chemistry: Dye-primer-amersham; 58 of reads
Chemistry: Dye-terminator Big Dye; 958 of reads
Assembly program: Phrap: version 0,960731
Consensus quality: 153620 bases at least Q40
Consensus quality: 153620 bases at least Q20
Insert size: 163000; agarose-fp.
Insert size: 162680; sum-of-contigs
                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 164180)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 17, clone RP11-550K23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 24, 2000 this sequence version replaced 91:5819142.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
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Outlity coverage

NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
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.00.0%; Pred. No. 0.27;
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4: gap of unknown length
4: gap of unknown length
5: contig of 1151 bp in length
5: contig of 1151 bp in length
6: contig of 1151 bp in length
7: gap of unknown length
7: gap of unknown length
8: contig of 1341 bp in length
8: gap of unknown length
8: gap of unknown length
8: gap of unknown length
9: gap of unknown length
7: gap of unknown length
7: contig of 12985 bp in length
7: contig of 12985 bp in length
7: gap of unknown length
8: gap of unknown length
9: contig of 32123 bp in length
9: contig of 33123 bp in length
9: gap of unknown length
9: gap of unknown length
9: contig of 33123 bp in length
9: gap of unknown length
9: contig of 32123 bp in length
                                                                                                                                                                                                                                                                                                                                   Insert sizė: 182000; agarose-fp
Insert size: 182375; sum-of-contigs
Quality coverage: 9 02 in 020 bases; agarose-fp
Quality coverage: 9.22 in 020 bases; sum-of-contigs
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44555 c 43725 g 45076 t 1011 others
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Sequencing vector: plasmid; 16%
Chemistry: Dye-primer ET; 84% of reads
Chemistry: Dye-terminator Big Dye; 16% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 177386 bases at least Q40
Consensus quality: 178778 bases at least Q30
Consensus quality: 179583 bases at least Q20
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/db_xref="taxon:9606"
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SEQUENCE, 16 unordered pieces.
ACO09837.2 GI:7321653
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Best Local Similarity 100.
Matches 22; Conservative
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source

FEATURES

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EDMANTON SEPTIONS

EDMANTON

EDMANTO
                                  AC031980 169913 bp DNA HTG 03-APR-2000
Homo sapiens clone RP11-330M20, WORKING DRAFT SEQUENCE, 44
unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                              AC031980.1 GI:7387341
                      RESULT 14
AC031980/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                        ORGANISM
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KEYWORDS
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JOURNAL
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                                                             41064 41133 gap of 7 100 bp 41164 50071; gap of 8908 bp in length 50072 50171; gap of 100 bp 50172 50171; gap of 100 bp 60778 60877; contig of 1060 bp in length 60878 6777; contig of 10868 bp in length 72746 72845; gap of 100 bp 72846 82971; contig of 10126 bp in length 82972 813071; gap of 100 bp 82972 813071; gap of 100 bp 103188 103287; contig of 20116 bp in length 103188 103287; contig of 20116 bp in length 113754 1131853; contig of 2010 bp 11809th 1131854 1131853; contig of 32327 bp in length 1131854 1131853; contig of 32327 bp in length
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33063: contig of 5750 bp in length
                   gap of 100 bp
33: contig of 7900 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="RP11-550K23"
clone_lib="RPCI-11 Human Male BAC"
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/note="assembly_fragment"
50172...60777
/note="assembly_fragment"
60878...72745
/note="assembly_fragment"
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/note="assembly_fragment"
83072. .103187
/note="assembly_fragment"
103288. .131753
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'note="assembly_fragment"
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/note="assembly_fragment"
27314. .33063
/note="assembly_fragment"
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'note="assembly_fragment"
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note-"assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .164180
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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100.0%; Pre
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                                            41063
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Query Match

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11095: gap of 1107 bp in length 106 1106 pp 13665: contig of 1270 bp in length 66 14829: contig of 106 pp 109 pp 1
                                                    contig of 1345 bp in length contig of 1439 bp in length p of 100 bp in length contig of 1319 bp in length contig of 1319 bp in length contig of 100 bp in length
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3546: contig of 1877 bp in length
3646: gap of 100 bp
39296: contig of 2650 bp in length
39396: gap of 100 bp
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89640: contig of 4022 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14829: contig of 1064 bp in length
14929: gap of 100 bp
16577: contig of 1128 bp in length
16157: gap of 100 bp
17567: contig of 1410 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .00 bp
1410 bp in length
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19356: contig of 1689 bp in length
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30748: contig of 2566 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48. gap of 100 bp
52. gap of 100 bp
52. gap of 100 bp
34569: contig of 1617 bp in length
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43689: contig of 4293 bp in length
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47256: contig of 3467 bp in length
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51218: contig of 3862 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18: gap of 100 bp 54648: contig of 3330 bp in length
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contig of 3403 bp in length
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contig of 3785 bp in length
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contig of 5225 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                  of 100 bp contig of 1241 bp in length
                     1436 bp in length
                     contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58151:
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9788: con
8: gap of
10995: con
1437 1536: 2782 2881: C. 2782 2881: gap of 2882 4320: C. 4321 4420: gap 4421 4420: gap 4731 4420: gap 4731 420: gap 4731 420: gap 4731 420: gap 6940 7408 8449 834
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32852:
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HS339A18 132805 bp DNA PRI 23-NOV-1999 Human DNA sequence from PAC 339A18 on chromosome Xpli.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiee, DNA binding protein similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                            139327 139426: gap of 100 bp
139427 150444: contig of 11018 bp in length
150445 150544: gap of 100 bp
150545 158766: contig of 8222 bp in length
155767 158866: gap of 100 bp
158867 169913: contig of 11047 bp in length.
                         100 bp 121589; contig of 7820 bp in length 121590 121689; gap of 100 bp 120180 129185; contig of 7496 bp in length 129186 129285; gap of 100 bp 100 bp 129286 139327 139426; gap of 100 bp 100 bp 139327 139426; gap of 100 bp 100 bp 139427 150444
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   bp
bp in length
                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-330M20"
/clone_lib="RPCI-11 Human Male BAC"
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Pred. No. 1;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="assembly_fragment"
16158. 17567
/note="assembly_fragment"
17668. 19356
/note="assembly_fragment"
19457. 21798
/note="assembly_fragment"
21899. 23416
/note="assembly_fragment"
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1537. 2781
/note="assembly_fragment"
2882. 4320
/note="assembly_fragment"
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25630. 28082
note="assembly_fragment"
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/note="assembly_fragment"
/008. .8248
/note="assembly_fragment"
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note="assembly_fragment"
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[4930. .16057
7972: gap of
113669: contig of
                                                                                                                                                                                                                                  Location/Qualifiers
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ع: gap of
121589: م
680
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Best Local Similarity 100.0%; Pr
Matches 21; Conservative 0;
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HS339A18/C
LOCUS
DEFINITION
                                                                                                                                                                                                                                                   source
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repeat_region
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/note="MIR repeat: matches 162. 34 of consensus"

/note="MIR repeat: matches 162. 34 of consensus"

complement(/oin(<1185. .1322,1418. .1564,1666. .1845,

1944. .2129,5234. .5441,5593. .5675,7932. .8092,8186. .8444,

9091. .9329,9423. .9626,10948. .11060,11171. .11359,

/note="match D80000; similar to mitosis-specific

/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human chromosome X, constructed by the Sanger Centre chromosome X human chromosome X, constructed by the Sanger Centre chromosome X mapping group. Further information can be found at http://www.sanger.ac.ux/HGP/Chrx/
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
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/translation="EienfkSykgrQiigpporftaligpngsgkSnlmdalsfylge
/translation="EienfkSykgrQiigpporftaligpngsgkSnlmdalsfylge
rtshlryteldlihgapygkpaantarfysmyseegaedrffartyfggssextinn
kvyQihetseelekigilikarnflytpggavesiamknpprertalfeelsrsgelage
ydkrkremytaredyfofnythrkniaaferkeakoekreadrygklofyvyrQi
fklythefyeieklnkelasknykeiekdkramdkyedeleke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding
                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (05-SEP-1997) Chromosome X Project Group
(http://www.sanger.ac.uk/HGP/ChrX/) Sanger Centre, Hinxton,
Cambridgeshire, CBIO 15A, UK. E-mail enquires:
On Sep 9, 1997 this sequence version replaced 91:2213437.
IMPORTANT: This sequence is the entire insert of clone 339Al8.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The true left end of clone 339A18 is at 1 in this sequence. The true right end of clone 339A18 is at 132805.
339A18 is from the library RPCI3 constructed at the Roswell Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overlapping clone as we submit sequences with only a small
                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Mammalia;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="Xp11.1-Xp11.4"
/clone="Rp3-339A18"
/clone_lib="RpC1-3"
616. .669
/note="MIR repeat: matches 217. .156 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          773. 902
note="AluSx repeat: matches 294. .56 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/
Location/Qualifiers
                                                                                        DNA binding protein; KIAA0178; smc1; Xp11.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="KIAA0178"
/protein_id="CAB09784.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .132805
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
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                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Eutheria; Primates; Catarrhini
1 (bases 1 to 132805)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ncomplete repeat"
URE-B1, ESTS and STS
297054
                                                                 297054.1 GI:2370077
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                                                                                                                                                            Homo saptens
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KEYWORDS
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AUTHORS
TITLE
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DY LEVKPTDEKLREIKGAKLVIDVIRYEPPHIKKALQYACGNALVCDNVEDARRIAFG
GHQRHKTVALDGTLFQKSGVISGGASDLKAKARRWDEKAVDKLKEKKERLTEELKEQM
KAKRKEAELRQVQSQAHGLOMRLKYSQSDLEGTKTRHLALNLQ"
                                       QKADQDRLDLEERKKVETEAKIKQKLREIEENQKRIEKLEEYITTSKQSLEEGQKKLEG
ELTEEVEMAKRRIDEINKELNQVMEQLGDARIDRQESSRQQRKAEIMESIKRLYPGSV
YGRLIDLCQPTQKKYQIAVTKVLGKNMDAIIVDSEKTGRDCIQYIKEQRGEPETFLPL
IKEKDSELNOKRPOY IKAKENTSHK IKKLEAAKKSLONAOKHYKKRKGDMDELEKEMI
                                                                                                                                                                                                                                                   7352. 3530
/note="MER21B repeat: matches 790. 511 of consensus"
3534.
7note="MER21B repeat: matches 459. .6 of consensus"
4220. 4507
/note="Alusx repeat: matches 1. .286 of consensus"
7note="11s copies of 2 mer 96 % conserved"
5033. .5309
/note="MIR repeat: matches 20. .216 of consensus"
5967. .6007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7815. 7888
/note="MER46 repeat: matches 1. .72 of consensus"
7852. 7906
/note="MER46 repeat: matches 136. .84 of consensus"
9986. .10286
/note="AluSq repeat: matches 1. .303 of consensus"
10288. .10323
/note="18 copies of 2 mer 81 % conserved"
10514. .10703
/note="MER5A repeat: matches 189. .3 of consensus"
11602. .11874 repeat: matches 7. .300 of consensus"
11875. .12047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matches 752. .914 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2280. .2410
Anote-FiLAM_A repeat: matches 2. .132 of consensus"
2871. .3169
/note-"AluSx repeat: matches 300. .2 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-"AluJo repeat: matches 134. .302 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="FLAM_C repeat: matches 131. .1 of consensus" 13461. .13762
/note="AluSp repeat: matches 2. .303 of consensus" 14357. .14623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .206 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                               5967, .6007
/note-"MIR repeat: matches 108, .150 of consensus"
6087, .6182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matches 135. .45 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .296 of consensus;
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/note="AluSg repeat: matches 1. .131 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .261 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     matches 904. .980 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matches 1. .300 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matches 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                matches 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      incomplete repeat"
7303. 7467
/note-"MIR repeat: matches 84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 matches
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/note="MER42c repeat:
13146. 13276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5087. .6182
/note="AluJb repeat:
incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5690. .6993
/note="AluSq repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluSc repeat:
12882. .13044
/note="LIMB2 repeat:
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/note="AluJb repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7501. .7798
/note="AluSg repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="AluSq repeat:
2587. .12880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5519. .6688
note-"Alusx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  incomplete repeat" 6690. .6993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    incomplete repeat<sup>n</sup>
6519. .6688
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/note="MIR repeat: matches 126. .47 of consensus" <27448. .28738 /note="match: multiple ESTs; match: H65678 R15918 T10016 AA156357 N22744; match: W93355 AA250790 AA255562 H63636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                incomplete repeat"
21686. 21729
/note="22 copies of 2 mer 84 % conserved"
22895. 23176
/note="Alusx repeat: matches 3. 286 of consensus"
2387. 23514
/note="MIR repeat: matches 23. 149 of consensus"
23631. 23745
/note="MIR2 repeat: matches 133. 15 of consensus"
25064. 25189
/note="MIR2 repeat: matches 63. 176 of consensus"
25758. 2588
                                                                                                                                                                                                                           /note="AluSg repeat: matches 1. .300 of consensus"
16042. .16137
/note="AluSg repeat: matches 190. .285 of consensus;
16121. .16417
/note="Malk repeat: matches 88. .189 of consensus"
16433. .16732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         incomplete repeat.
20656. 20850
20656. 20850
incomplete repeat: matches 196. .1 of consensus;
10002. .20969
//ote="Li repeat: matches 4932. .4999 of consensus"
2102. .2124
//octe="Alux repeat: matches 1. .144 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                            /note="AluSx repeat: matches 1. .302 of consensus"
17427. .17604
/note="Match: Depeat: matches 39. .216 of consensus"
<19138. .24266
/note="match: 5' EST AA383258"
/note="AluJb repeat: matches 1. .295 of consensus"
20431. .20647
/note="AluJb repeat: matches 87. .301 of consensus"
/note="AluJb repeat: matches 87. .301 of consensus;
                                                                                         Incomplete repeat.
14952. 15251
700te-AluSx repeat: matches 1. .302 of consensus.
15332
700te-AluJb repeat: matches 1. .297 of consensus.
15735. 16034
/note="AluSg repeat: matches 298. .3 of consensus" (4512. .14749
                                                                 note-"AluJo repeat: matches 283. .1 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prim_transcript
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Query Match 3.6%; Score 20; DB 10; Length 132805; Best Local Similarity 100.0%; Pred. No. 3.8; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps

Search completed: September 3, 2000, 16:21:22 Job time: 21399 sec

sapien lus gall

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086445 planktothri

088099 planktothri

088099 planktothri

09813 pyrococcus

095613 chlamydia p

017460 schistosoma

024019 drosophila

092x31 caenorhabdi

092x31 caenorhabdi

092x31 arabidopsis

095404 homo sapien

08459 chlamydia t

077384 plasmodium

09449 arabidopsis

077371 plasmodium

191349 caenorhabdi

172877 synechocyst

092183 mus musculu

054377 lactococcus

092183 mus musculu

054377 lactococcus

092183 acenorhabdi

17287 synechocyst
                             028532 archaeoglob
039794 ebola virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 QETFCLFDIGQNFSNSQEHLDLLQQRIKQRSFPERKDEVSTEKTLGEPSETIVVSTDVAS 120
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O46616;
O46616;
O46616;
O46016;
O1-JUN-1998 (TEMBLE-1. 06, Created)
O1-JUN-1998 (TEMBLE-1. 06, Last sequence update)
O1-JUN-1998 (TEMBLE-1. 06, Last annotation update)
O1-JUN-1998 (TEMBLE-1. 06, Last annotation update)
INTERPHOTORECEPTOR MATRIX PROTEOGINCAN 150 (FRAGMENT).
Macaca fascicularis (Crab eating macaque) (Cynomolyus monkey).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
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TISSUE-RETINA;
TISSUE-RETINA;
KUEHN M.H., HAGEMAN G.S.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AR047491; AAC03788.1; -.
NON_TER 1 1
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Pred. No. 2.5e-77;
; Mismatches 0;
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                                                       086445
08809
08809
092613
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ilarity 100.0%; Pr
Conservative 0;
185 AA;
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Best Local Similarity
Matches 185; Conserv
 ADSQS 185
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NON_TER
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SEQUENCE
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095094 homo saplen
P70628 rattus norv
006979 bacillus su
089717 homo saplen
085467 patteurella
097460 homo saplen
032269 bacillus su
089799 mus musculu
004494 arabidopsis
097970 thermotoga
094701 bacillus su
094701 bacillus su
09547 caenorhabdi
01560 caenorhabdi
01560 caenorhabdi
01452 schizosacch
                                                                                                    ; Search time 66.18 Seconds
(without alignments)
193.817 Million cell updates/sec
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homo sapien
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                                                                                                                                                                              950
1 IFFPNGVKVCPQESMKQILA......ELSISLINQRFKAELADSQS 185
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                                          protein search, using sw model
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043686
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fung1:*
sp_human:*
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sp_unclassified:*
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Potal number of

Searched:

Minimum DB Maximum DB

Database

Title: Perfect score:

Sequence:

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Run

Scoring table:

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9 Gaps

950 8855 897.5 897.5 875.5 875.5 885.5 885.5 885.5 885.5 885.5 885.5

Result No.

82.5 82.8 82 81 81 80

79.5

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Gaps

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RESULT 3686 OV 3686 OV

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SEQUENCE FROM N.A.
MEDLINE; 97038366.
WANG X., BROWNSTEIN M.J., YOUNG W.S.;
Sequence analysis of FG10.2, a gene expressed in the pineal gland and the outer nuclear layer of the retina.";
Brain Res. Mol. Brain Res. 41:269-278(1996).
EMBL; U76717; AAC52891.1;
PFAM; PF01390; SEA; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                    93.2%; Score 885; DB 4; Length 797; 90.8%; Pred. No. 8.8e-71; live 9; Mismatches 8; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                           797 AA; 89387 MW; 2369FDEA CRC32;
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AAC68835.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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P70628
01-FEB-1997 (TrEMBLrel. 02, C
01-FEB-1997 (TrEMBLrel. 02, L
01-MAY-1999 (TrEMBLrel. 10, L
PG10.2.
                                                                                                                                                                                                                                                     AAC68835.1;
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Best Local Similarity 90.8'
Matches 167; Conservative
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Best Local Similarity
Matches 67; Conserv
                                                                                                              AF017770; AF017771; AF017772; AF017772;
                                                           AF017768;
AF017769;
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                                 AF017767;
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SEQUENCE 13
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Receptor.
SEQUENCE
                                                                                                                                       EMBL;
EMBL;
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EMBL;
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EMBL;
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MEDLINE; 98358139.
FELBOR U., GEHRIG A., SAUER C.G., MARQUARDT A., KOHLER M., SCHMID WEBER B.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TREMBLrel. 10, Last sequence update)
101-MAY-1999 (TREMBLREL. 10, Last annotation update)
1NTERPHOTORECEPTOR MATRIX.
1PM150
1PM150
1PM150
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cenomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a cand Gq-1nhted retinopathies."; Cytogenet. Cell Genet. 81:12-17(1998).

EMBL; AF01776; AAC68835.1; CINED.
EMBL; AF01776; AAC68835.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 771;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TSSOR-FRINA;
KUEHN M.H., HAGEMAN G.S.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. *
EMBL; AF047492; AAC03789.1; -.
FFRAN; PFO1390; SEA; 1.
SEQUENCE 771 AA; 86372 MW; 1580AF90 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.2%; Score 885; DB 4; Length 77
90.8%; Pred. No. 8.4e-71;
tive 9; Mismatches 8; Indels
                                                                                                        043686 PRELIMINARY; PRT; 771 AA. 043686; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-MAY-1999 (TrEMBLrel. 10, Last annotation update) INTERPHOTORECEPTOR MATRIX PROTEOGLYCAN 150. IMPG1.
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Best Local Similarity 90.8
Matches 167; Conservative
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26; Mismatches
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NON_TER 1
SEQUENCE 737 AA, 80758 MW;
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26.1%
Matches 31; Conservative
                                                                                                                                                                                                                                                                        153 R----ETELAVSEE 162
                                                                                                                                                                                                                                                                                                                       267 RIETQGHETRLSVADE 282
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01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
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AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
BORKISS K., BONGSIER C.V., CALLWELL B., CAPUNOU V., CARTER N.M.,
CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
BROUILET S., BRUNGHI C.V., FABRET C., EHRICHS S.D., EMMERSON P.T.,
A DENTION K.D., ERRINGTON J., FABRET C., ERRARIE E., FOULGER D.,
A HILBERT H., HOLSAPPEL S., HORONO S., HALLOM M.F., ITAYA M., JONES L.,
A HILBERT H., HOLSAPPEL S., HORONO S., HULLO M.F., ITAYA M., JONES L.,
A KOBAYASHI Y., KOETTER P., KONINGSTEIN G., KROGH S., KUMANO M.,
A KOBAYASHI Y., MALLADO R.P., LARDINOIS S., LAUBER J., LAZAREVIC V.,
A KOBAYASHI Y., MALLADO R.P., MIZUNO M., MOESTL D., NARAI S., NOBACK M.,
A RESECAN B., PORTILLE D., PORWOLLIK S., PARKS S.H.,
A RESECAN B., PORTILLE D., PORWOLLIK S., PARK S.H.,
A RESECAN B., PORTILLE D., PORWOLLIK S., SIDAN B.S.,
A RIGGER M., RYVOLTA C., ROCHA E., RACHORTE R., SIDAN B.S.,
A SATO T., SCANLAN E., SCHEICH S., SCHROFTE R., SHIN B.S.,
A SOROKIN A., TARCONI E., TAKARASHI H., TAKARANU K.,
A TAKEUCHI M., TAMAKOSHI A., TAKARASHI H., TAKARAKI K.,
A TAKEUCHI M., TAMAKOSHI A., TAKARASHI H., TAKARAKI K.,
A TAKEUCHI M., TAMAKOSHI T., TAKARASHI H., TAKARAKU K.,
A TAKEUCHI M., TAMAKOSHI T., TAKARASHI H., TAKARAKI K.,
A TOSTON B., TAKARASHI T., WEDLER H., WEDLER H.,
"The complete genome sequence of the gram-positive bacterium Bacillus subtilis: ",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                       01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 40.2 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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Pred. No. 1.9;
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SEQUENCE 356 AA; 40180 MW; 2940FA74 CRC32;
                                                                                                                                                                                                                                                                        PRT;
                                                                                                                  237 AEFSIQLLGRQYSEELRDPSS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 294043; CAB08063.1; -.
                                                                             165 VELSISLINQRFKAELADSQS
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                                                                                                                                                                                                                                                                        PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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MEDLINE; 98044033
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TISSUE-BRAIN;
MEDLINE; 99246053.
MEDLINE; 99246063.
MAGASE T., ISHIKAWA K., SUYAMA M., KIKUNO R., HIROSAWA M.,
NAGASE T., ISHIKAWA K., KOTANI H., NOMURA N., OHARA O.;
MIYAJIMA N., TANNKA A., KOTANI H., NOMURA N., OHARA O.;
"Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA RES. 6:63-70(1999).
                                                                                                                                                                                224 ------TLHVPPNAVQISSDQKWLSF------VVEQILFNALKYSKQGVGDPIII 266
                                                                             97 DEVSTEKTLGEPSETIVVSTDVASVSLGPFPVTPDDTLLNEILDNALNDTKM----PTTE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 QNFSNSQEH-----LDLLQQRIKQRSFPERKDEVSTEKTLGEPSETIVVSTDVASV 121
Gaps
                                                 37 EAYRIFLDRIPDIGEYQDWVSFCQQETFCLFDIGQNFSNSQEHLDLLQQRIKQRSFPERK 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 QALSNSEEEKKGVAASLIAPLLPEGIKEEEERWRRKVICKEEPVSEVKETSTTVEEATTI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 SLGPFPVTPDDTLLNEILDNALNDTKMPTTERETELAVSEEORVELSISLINQRFKAEL 180
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CHUNG J.Y., ZHANG Y., ADLER B.;
CHUNG J.Y., ZHANG Y., ADLER B.;
"The capsule blossynthetic locus of Pasteurella multocida A:1#.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF067175; AAC67255.1; -.
35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pasteurella multocida.
Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
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26.1%; Pred. No. 6.2;
tive 20; Mismatches 50; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
KIAA1014 PROTEIN (FRAGMENT).
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Last annotation update)
40;
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SEQUENCE FROM N.A.
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                                                                                                                                            60 QQETFCLFDIGQNFSNSQEHLDLLQQRIKQRSFPERKDEV-----STEKTLGEP 108
                                                                                                                                                                        137 SKKLSVNFDSVSGIATLNIRAFDPKEAQQINQELLKQGEYLINRLNERARKDTVMFAELA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------AVPAAGD--ESISSLSELVRAMHPY 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 CLFDIGQNFSNSQEHLDLLQQRIKQRSFPER---KDEVSTEKTLGEPSETIVVSTDVASV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 98290545.
NAGASE T., ISHIKAWA K., MIYAJIMA N., TANAKA A., KOTANI H., NOMURA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 CPQESMKQILASLQAYYRLRVCQEAVWEAYRIFLDRIPDTGEYQDWVSFCQQ----ETF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Prediction of the coding sequences of unidentified human genes. In the complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:31-39(1998).
                                                                                                                                                                                                                              109 SETIVVSTD----VASVSLGPFPVTPDDTLLNEILD-----NALNDTKMPTTERETELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 CL----PNLTHLASLEDELQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPVV---VROV
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                                                                                                   27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                            Length 378;
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                                                                                                     59; Indels
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Last sequence update)
Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
KIAA0595 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.0%; Score 85.5; DB 4; I
26.6%; Pred. No. 25;
tive 21; Mismatches 57;
                                                            5;
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SF06D1F6 CRC32;
                                           9.0%; Sco...
26.2%; Pred. No. 4....
'''e 24; Mismatches
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                                                                                                                                                                                                                                                                                                              159 VSEEQR--VELSISLINQRFKAELADSQS 185
                                                                                                                                                                                                                                                                                                                                        197 VSEAEKKVTETSSALSEYRIKNGVFDLQS 225
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43245 MW;
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                                                        Query Match
Best Local Similarity 26.2<sup>§</sup>
Matches 39; Conservative
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Best Local Similarity 26.6'
Matches 46; Conservative
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378
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SEQUENCE
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RATIOR S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M., BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M., COLONIE K.M., FUGITA Y., ENARRASI E., FOULGER D., CALLERON P.T., FARTIZ C., FUJITA M., FUGITA Y., FORM S., EMMERSON P.T., FARTIZ C., FUJITA M., FUGITA Y., FORM S., GRALIZI B., GALLERON N., GILIEBTR B., GALLIZI A., GALLERON N., GILIEBTR B., GORNES D., GOLIGHILY E.J., GRANDI G., GUY B.J., HAGA K., HAIECH J., HARWOOD C.R., HENAUT A., ANDRAWATA D., KASAHARA Y., KLERR-BLANCHARD M., KLEIN C., ANDRAWATA D., KASAHARA Y., KLERR-BLANCHARD M., KLEIN C., MEDIGUE C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOLDO B., LAZAREVIC V., PAGNI M., KARAMATA D.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 299122; CAB15573.1; -.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z99122; CAB15573.1; -.
EMBL; AF015609; AAB94867.1; -.
Hypothetical protein.
SEQUENCE 226 AA; 25134 MW; D0DD4C8E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.9%; Score 85; DB 2;
25.2%; Pred. No. 2.7;
tive 26; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 LEGESVSEDSKVD-----KERFLYELKNTQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 ----AVSEEQRVELSISLINQRFKAELADSQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Conservative
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98 EVSTEKTLGEPSETIVVSTDVASVSLGPFPVTPDDTLLNEILDNALNDTKMPTTERETEL 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----IDTTOGNESNSQEH-----LDTTQQRIKQRSFPERKDEVSTEKTL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            935 -NNSKNVVIKY------IDELIKNLVDNLDKLNYMDFAVTKRYSGKYVSIDN 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 SLQAYYRLRVCQEAVWEAYRIFL-DRIPDIGEY------QDWVSFCQQETFCLFD 68
                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TREMBLREL. 10, Last annotation update)
01-NOV-1999 (TREMBLYTE DIA POLYMERASE, CHORISTONEURA BIENNIS ENTOMOPOX VIRUS DPOL HOMOLOG (VACCINIA E9L), SIMILAR TO SW:P30319.
                                                                                                                                                                                                                                                                                                                                                                                                    Melanoplus sanguinipes entomopoxvirus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
                                     447 ANSTAKDLSGKIQEVKMDEDVEGDGLNPEDIQEEDTV--EDSDSISNEREIKNAEEIKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 GEPSETIVVSTDVASVSLGPFPVTPDDTLLNEILDN--ALNDTKMPTTERETELAVSEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         889 IINYDTLEAKIESKGTSLIKRDYSNFHKHHYKTIIEIIQKSIENKN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., ROCK Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACITYTY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE + DNA(N).

EMBL; AFO613866; AAC97837 1; -.

EMBL; SF00116; DNA_POLYMERASE_B; 1.

DNA_dlrected DNA_POLYMERASE_B; 1.

SEQUENCE 1079 AA; 127406 WW; 3C26B08D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., ROCK "The genome of Melanoplus sanguinipes entomopoxvirus."; J. Virol. 73:533-552(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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18.1%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                   1079 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Mismatches
                                                                                                                          526
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                                                                                                                                                                                                                                   PRT;
                                                                                                        158 AVSEEQRVELSISLINQRFKAELADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 18.18
Matches 35; Conservative
                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 RVELSISLINQRF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||::: | ::
980 IIELTVNKFNAKY 992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Q9WYJ0;
                                                                                                                                                                                                                                   09YW56
                                                                                                                                                                                       RESULT 12
Q9YW56
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STRAIN-CV. COLUMBIA;
VYSOTSKAIA V.S., OSBORNE B.I., TORIUMI M., YU G., OJI O., SHEN Y.K.,
VYSOTSKAIA V.S., OSBORNE B.I., TORIUMI M., YU G., OJI O., SHEN Y.K.,
ARAUJO R., AU M., BUEHLER E., CONWAY A.B., CONWAY A.R., DEWAR K.,
FENG J., KIM C., KURTZ D., LI Y., SHINN P., SUN H., DAVIS R.W.,
ECKER J.R., FEDERSPIEL N.A., THEOLOGIS A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, ACO00132; AAB6072811: -
EMBL, ACO00132; AAB6072811: -
EMBL, COSFSB13 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 DTGEYQDWVSFCQQETFCL----FDIGQNFSNSQEHLDLLQ---QRIKQRSFPERK---D 97
                                                                                                                                                                                                                                                             MEDLINE; SOLESTAY.

GAO Z., GARBERS D.L.;
GAPERS D.L.;
"Species diversity in the structure of zonadhesin, a sperm-specific membrane protein containing multiple cell adhesion molecule-like domains.";
J. Biol. Chem. 273:3415-3421(1998).
EMBL; U97068; AAC26680.1;
HSSP; P56215; 1ACW.
PFAM; PF00094; vwd; 4.
SEQUENCE 5376 AA; 579899 WW; F362DEFF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, euphyllophytes, Spermatophyta, Magnollophyta; eudicotyledons; core eudicots, Rosidae, eurosids II; Brassicales, Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 TLENEILDNALNDTKMPTTERET------ELAVSEEQRVELSISLIN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                     Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1997 (TremBirel. 04, Created)
01-JUL-1997 (TremBirel. 04, Last sequence update)
01-MOV-1999 (TremBirel. 12, Last annotation update)
SEQUENCE OF BAC F21M12 FROM ARABIDOPSIS THALIANA CHROMOSOME
COMPLETE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.7%; Score 83; DB 10; Length 947; Best Local Similarity 23.3%; Pred. No. 23; Matches 34; Conservative 32; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Indels
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.8%; Score 84; DB 11;
Best Local Similarity 23.7%; Pred. No. 1.6e+02;
Matches 27; Conservative 23; Mismatches 38.
PRT; 5376 AA
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                                           Created)
                                       (TrEMBLrel. C
(TrEMBLrel. C
(TrEMBLrel. 1
PRELIMINARY;
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                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 98123114.
                                       01-NOV-1998 (
01-NOV-1998 (
01-NOV-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis
                                                                                                        ZONADHESIN.
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004494
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CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 LKKEI 197
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095347;
01-MAY-1999
01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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095347
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ف
                                                                                  NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
MCDOMALD L., UTTERBACK T.R., MALEK J.A., LINERS K.D., GARRETT M.M.,
STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALEBERG S.L.,
SMITH H.O., VENTER J.C., FRASER C.M.;
"Evidence for lateral gene transfer between Archaea and bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 SQEHLDLLQQRIKQRSFPERKDEVSTEKTLGEPSETI----------VVSTDVA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 AQEDYKTSQELFKKNLISE-NDLKDSELTLEEASNNLLSAQKDLEEAQKDYEEIFSVEVS 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 SVSLGPFPVTPDDTLL--NEILDNALNDTKMPTTERETELAVSEEQRVELSISLINQRFK 177
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HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.
SMITH H.O., VENTER J.C., FRASER C.M.;
SUDMITTED (JUN-1999) to the EMBL/Genbank/DDBJ databases.
HYPOThetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Gaps
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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01-07-1998 (TrEMBLrel. 08, Last annotation update)
CELL DIVISION CYCLE CDC48 HOWOLOG (YJOB PROTEIN).
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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328 AA; 37575 MW; 1D029EE8 CRC32;
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Bacteria; Thermotogales; Thermotoga
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RIVOLTA C., SOLDO
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MEDLINE; 98044033
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136 AVNDEKMRAFLEGVRPRLWEKSKRKVTVFTDGDGGTSREQEAIVREVQRSQV---IMNPL 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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19.5%; Pred. No.
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DA SILVA E., KARAMATA D.;
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CHROMOSOME-ASSOCIATED PROTEIN-E.

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MISSUB-TERATOCARCINOMA;

MEDLINE; 99007239.

SCHMIESING J.A., BALL A.R. JR., GREGSON H.C., ALDERTON J.M., ZHOU S., YOKOMORI K.;

"Identification of two distinct human SMC protein complexes involved in mitotic chromosome dynamics.";

Proc. Natl. Acad. Sci. US.A. 95:12906-12911(1998).

EMBL; AF092563; AAC72360.1; -.

SEQUENCE 1197 AA; 135780 MW; 9E999CBF CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.5%; Score 81; DB 4; Length 1197;
Best Local Similarity 24.2%; Pred. No. 47;
Matches 23; Conservative 24; Mismatches 32; Indels 16; Gaps
                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AEPLSKPWLEDDDSLLPAETEDRKLVLVDKWDSTDGISKHSKYEHDDRSTHPPEEEPL
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1 (basas: 1 to 3989)
Acharya,S., Foletta,V.C., Lee,J.W., Rayborn,M.E., Rodriguez,I.R., Sung,W.S. 3rd and Hollyfield,J.G.
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Foletta, V.C. and Young, W.S.
Direct Submission
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Bethesda, MD 20892-4068, USA
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	DD 1209 AACACCCAAAGTTCAAGTCTTCAGGCAACGCCGTCATTTTTTTT	80 0 4	Qy 1626 ttagaggttagcagcttgactctcattctgtcacccggcagtgcttcagactg 	വ യ പ	9 Qy 1806 cctgtgccaaaagaaacaataccatccatggaagactctgatgtgtccttaa 	Oy 1866 ccatatctgacctcttctataccttttggcttggactcttgacctccaaagtcaaa 5	1926 caattaaagtgagccctttcctgccagatgcatccatggaaaagagttaatattt 	Oy 1986 gqtgqtttegqgqtttegqgqaaagqttqqtttattqttqttcqttgqtqtqtq 65   De 1809 GGTGGTTTAGGTTCAGGGTCTGGCCAAAAGGTAGATCTGATTACTTGGCCATGGAGTGA 88   Ov 2046 arttcattagagagagagagagagagagagagagagagagag	1869 ACTICATCAGAG	1929	Oy 2166 gaccaaattagtaagcactcaaaatagacagatccacacaca	222b gaagagoctcttagtgggoctgctgtgcocatcttcgcagatactgcagartactgcagartactgcagartactgcagartactgcagartactgcagartactgcagartactgcagartactgcagartactgcagartactgcagartactgcagartactactactactactactactactactactactactact	65 Db 2109 TCTCTAACCCTCCCAAGCACATATCAGAAGTACCTGTGTGTG	Oy 2346 aaagcacctcttatactgacatctgtagcaatctctgcctctactgataaatcagatca
atch  cal Similarity 99.8%; Pred. No. 0;  3824; Conservative 0; Mismatches 6; Indels 0; Gap  ctgatagaagagactttccatcattaacagcacaaacttatctatagagagatc 3	306 caagaacccaagaffcagtttcttctctgcctgaagaatcaacagacctttctctc 36	aggoggagatctattctgtttcctaatggagtgaaaatctgcccagatgaaagtgttgca 4.	GAGGCTGTGGCAAATCATGTGAAGTATTTTAAAGTCCGAGTGTGTGT	606 aatttgtgtgaggatggagtcacaagtatatttgaaatgggcacaaattttagtgaatct 66	SCAGO 5 ctete 7	6 agtgiticcacaticcagaggiggacgcctatgaaggigcctcagagagagagttggaaagg	agagtattagcaatgaaattgagaatgtgatagaagaagccacaaaaccagca	906 ggtgaacagattgcagaattcagtatccaccttttggggaagcagtacagggaagaacta 96 	966 caggattcctccagctttcaccaccagcaccttgaagaatttattt	1026 aatgcatttactgggttaccaggctacaaggaaattcgtgtacttgaatttaggtcccc 10	1086 aaggaaaatgacagtggcgtagatgtttactatgcagttaccttcaatggtgaggccatc 11	1146 agcaataccacctgggacctcattagccttcactccaacaaggtggaaaaccatggcct 12	1206 gtggaactggatgataaacccactgttgtttatacaatcagtaacttcagagattatatt 12 	ctgat 1

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          gaatcagagagagtttggacaagaacttcttccctagagaaattgtccagagacatattg
                                                                 GAATCAGAGAGTTTGGACAAGAACTTCTTCCCTAGAGAAATTGTCCAGAGACATATTG
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Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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  cccgtgatcataggcatcactattgcctccgtggttggacttcttgtcatcttttctgct
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                                                  3309 CCCGTGATCATAGGCATCACTATTGCCTCCGTGGTTGGACTTCTTGTCATCTTTTCTGCT
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Homo sapiens, clone RP11-571M4
Unpublished
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HTG; HTGS_PHASE1; HTGS_DRAFT
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Submitted (11-FBB-2000) Whitehead Institute/MIT Center for Genome Submitted (11-FBB-2000) Whitehead Institute/MIT Center for Genome Seearch, 320 Charles Street, Cambridge, MA 02141, USA ON MAT 3, 2000 this sequence version replaced 91:7139729.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator B19 bye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 17829 bases at least Q40
Consensus quality: 17329 bases at least Q30
Consensus quality: 174972 bases at least Q20
Insert size: 180000; agarose-fp
Insert size: 176164; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; sum-of-contigs
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of 2872 bp in length
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of 2229 bp in length
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contig of 6622 bp in length
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of 8406 bp in length
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of 4150 bp in length
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35767: contig of 6013 bp in length
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14245: contig
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68982: contig
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29654: cont
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1926 GGATTAGCCAATGTTGAAGAGTCAGAAGATTTTCTTTCTATTGATTCATTGCCTTCAAGT 1985
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100198 100297: gap of 100 bp 114772: contig of 14475 bp in length 114773 114872: gap of 100 bp 114873 132014: contig of 17142 bp in length 132015 132114: gap of 100 bp 132115 156372: contig of 1258 bp in length 156373 156472: gap of 100 bp 156373 1
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note="assembly_fragment"
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/note-"assembly_fragment"

4551. .6779

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6880. .9955

/note-"assembly_fragment"

10096. .1445

/note-"assembly_fragment"

14346. .17761
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35868. 44494
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24168. .29654
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88141. .100197
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100298. .114772
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156473. .178064
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29755. .35767
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Best Local Similarity 99.8
Matches 1257; Conservative
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                             ttaacatcttcaccatatctgacctcttctataccttttggcttggactccttgacctcc
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Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 77043)

Saltran,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 3, clone RP11-66311

Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boukhgalter,B. Brown,A., Burkett,G., Collins,S., Campoplano,A., Castle,A., Choepel,Y., Choangelo,M., Collins,S., Collymore,A., Cooke,P., DeArrellano,K., Dewar,K., Data,J.S.,

Campoplano,A., Castle,A., Choepel,W., Prizellano,K., Dewar,K., Data,J.S.,

Collymore,A., Cooke,P., DeArrellano,K., Dewar,K., Data,J.S.,

Collymore,A., Cooke,P., DeArrellano,K., Dewar,K., Data,J.S.,

Collymore,A., Cooke,P., DeArrellano,K., Conlins,S.,

Collymore,A., Cooke,P., DeArrellano,K., Anderon,L., Karatas,A.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Rowland,J.C., Illev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,

Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,

Kandrin,J., Meneus,D., Mihova,T., Miranda,C., Menga,V., Morrow,J.,

Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Connell,P.,

O'Nell,D., Ollvar,T.M., Ollver,J., Peterson,K., Plerre,N.,

Standos-Rossand,C., Schauer,S., Severy,P., Spencer,B.,

Standy-Chomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Young,G., Zahoun,J., Valmaer,A. and Zody,M.,

Submitted (01-APR-2000) Whitehead Institute/MIT Center for Genome Research, 30 Charles Street, Cambridge, Ma 02141, USA

All repeats were identified using RepeatMasker: html

Center: Miltehead Institute/MIT Center for Genome Research, Spiecer, P. (1996-1997)

Http://ftp.genome.washington.edu/Rw/RepeatMasker: html

Center: Miltehead Institute/MIT Center for Genome Research, Spiecer, Washington.edu/Rw/RepeatMasker: Html

Center: Miltehead Institute/MIT Center for Genome Research, Spiecer, Washington.edu/Rw/RepeatMasker:
                                    3126 GATCTGTTAATAAAACTCCTTGGAGTATAAAGCCCTGGAGCAAAGATTCTTAGAATTG 3185
                                                                                                                                                                                                                                                                               NA HTG 01-APR-200 clone RP11-663C11 map 3, LOW-PASS
2934 gatotgtttaataaaaactoottggagtataaagooottggagcaaagattottagaattg
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* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* Will be sequenced to completion. In the event that

* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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1613: contig of 750
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Center clone name: 663_C_11
                                                                                                                                                                                                                                                                      DNA
3 c
                                                                                                                                                                                                                                                          Homo sapiens chromosome SEQUENCE SAMPLING.
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bp in length

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57: gap of 100 bp
18237: contig of 780 bp in length
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23535: contig of 778 bp in length
           in length
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10318: contig of 773 bp in length
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p of 100 bp
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14719: contig of 764 bp in length
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24435: contig of 800 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25430: gap of 100 bp 26223: contig of 793 bp in length
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27957: contig of 765 bp in length
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30558: contig of 771 bp in length
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                                                                                                                           764 bp in length
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                                                                                                                                                                                                                                                                                                             796 bp in length
                                                                                                                                                                                                                                                                                                                                                         83 bp in length
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                                                                                                                                   100 bp
of 750 bp 4
                                           100 bp
f 796 bp 1
100 bp
f 745 bp 1
100 bp
                                                                                                     f 780 bp 1
100 bp
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11205: contig of 787 bp
11305: gap of 100 bp
12077: contig of 772 bp
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contig of 779 bp
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3060 13855: contig of 7
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contig of
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25330: con+4
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28832:
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12959:
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32305:
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5703 16478: con
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17357: con
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21786: con
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22657: con'
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27092: con
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15602: con
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20899: con
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                                                    4343: gap c
5088: c
5188: gap o
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7682:
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1430 ggataatacctttcaagctgcatggcctcagcagatgaatccatcaccagcagtattcc 1489 1490 accacttgatttcagctctggtcctccctcagccactggcagggaactctggtcagaaag 1549 24639 GGATAATACCTTTCAAGCTGCATGGCCCTCAGCAGATGAATCCATCACCAGCAGTATTCC ö Length 77043; 33278 34048: contig of 771 bp in length 34049 34148: gap of 100 bp 34934: contig of 786 bp in length 34935 35034: contig of 786 bp in length 35035 35793: contig of 759 bp in length 35693: gap of 100 bp 35894 35983: gap of 100 bp 35645; gap of 100 bp 37545: contig of 765 bp in length 3659 37545: gap of 100 bp 37546, 37645: gap of 100 bp 40280 40179: contig of 783 bp in length 40280 40179: contig of 783 bp in length 40280 41157: gap of 100 bp 4120 42801: contig of 762 bp in length 41920 42801: contig of 762 bp in length 41920 42801: contig of 781 bp in length 41920 42801: contig of 781 bp in length 42801 42900: gap of 100 bp 42801 42900: gap of 100 bp 42801 43777: contig of 771 bp in length 42801 43901: gap of 100 bp 42801 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43901 43 42801 42900: gap or 100 bp 42801 42901 42901 42901 42901 42901 43677: gap of 100 bp 44578 44559 contig of 777 bp in length 44550 44649; gap of 100 bp 44650 45427: contig of 778 bp in length 4520 4521; gap of 100 bp 4522 46421; gap of 100 bp 4532 46421; gap of 100 bp 4532 46421; gap of 100 bp 47302 48095: contig of 794 bp in length 47302 48095: contig of 794 bp in length 48096 48195: gap of 100 bp 48196 48195: contig of 794 bp in length 48096 48195: gap of 100 bp 48196 48195: contig of 784 bp in length 48927 49927 contig of 784 bp in length 49927 50778: contig of 771 bp in length 51650 51749: gap of 100 bp 51650 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51750 51 Indels couring of 743 bp under the control of 743 bp under the control of 778 bp in length 57726: contig of 753 bp in length 7826: gap of 100 bp 100 bp 8734 gap of 100 bp 59545: contig of 811 bp in length 9645: gap of 100 bp 1 794 bp ---100 bp ---753 bp in length 101: gap of 100 bp 55979: contig of 778 bp in length 179: gap of 100 bp 56873: contig of 794 bp in length 7.3%; Score 306; DB 71; 100.0%; Pred. No. 7.4e-166; ive 0; Mismatches 0; 10 July contig of 75 gap of 60513: contig of 7 Query Match 7.3 Best Local Similarity 100. Matches 306; Conservative 59546 59645: 59646 6041 60414 60513: 57826: 55202 559 55980 56079 56973 ద à à

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NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                     Chemistry: Dye-terminator Big Dye; 1008 of reads Assembly program: Phrap; version 0.966731 consensus quality: 168227 bases at least Q40 consensus quality: 173239 bases at least Q30 consensus quality: 174972 bases at least Q20 insert size: 180000; agarose-fp losert size: 176164; sum-of-contigs Quality coverage: 4.5 in Q20 bases; sum-of-contigs Quality coverage: 4.6 in Q20 bases; sum-of-contigs
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                                                Sequencing vector: M13; M77815; 100% of reads
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1479 1578: gap of 100 bp
1579 4450: contig of 2872 bp in length
4451 4550: gap of 100 bp
6780 6879: contig of 2229 bp in length
6780 6879: contig of 3116 bp in length
6880 9995: contig of 3116 bp in length
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'note="assembly_fragment"
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/note-"assembly_fragment"
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/note="assembly_fragment"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-571M4"
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49216: con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC023311 178064 bp DNA HTG 03-MAR-2000
Homo sapiens clone RP11-571M4, WORKING DRAFT SEQUENCE, 20 unordered
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Teleostomi;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (11-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2000 this sequence version replaced 91:7139729.
                                                                                                                                                                                                                                                                                                                                                                                                             24819 CICITCCCCAGAGGIIITAGAGGIIAGCAGCIIGACICIICAITCIGICACCCCGGCAGI 24878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24879 GCTTCAGACTGGCTTGCCTGTGGCTTCTGAGGAAAGGACTTCTGGATCTCACTTGGTAGA 24938
24699 ACCACTTGATTTCAGCTCTGGTCCTCCTCAGCCACTGGCAGGGAACTCTGGTCAGAAAG 24758
                                                                                           1550 tcctttgggtgatttagtgtctacacacaaattagcctttcctcgaagatgggcctcag 1609
                                                                                                                                                                                                                                                                                                            1610 ctcttccccagaggttttagaggttagcagcttgactcttcattctgtcaccccggcagt 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1670 gcttcagactggcttgcctgtggcttctgaggaaaggacttctggatctcacttggtaga 1729
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Center: Whitchead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                      24759 TCCTTTGGGTGATTTAGTGTCTACACACAAATTAGCCTTTCCCTCGAAGATGGGCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-571M4
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Center clone name: 571_M_4
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 184655)
Bliren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 4, clone RP11-144C15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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     SEQUENCE, 12 unordered pieces.
                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT
                                                         AC009581.3 GI:6563621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36625 ACCACTIGALTICAGCICTGGICCTCCCTCAGCCACTGGCAGGGAACTCTGGICAGAAAG 36566
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Homo sapiens chromosome 4 clone RP11-144C15 map 4, WORKING DRAFT
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a 33224 c 33032 g 53564 t
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88141. .100197

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10096. .14245
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/note="assembly_fragment
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/note="assembly_fragment
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 77043)
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Campopiano,A., Castle,A., Chopel,Y., Calangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 tttgaaaggacaaccatttttctttccgctaatttataatggttttgaagtggttgttca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 6.4%; Score 268; DB 42; Length 184655; Similarity 100.0%; Pred. No. 1e-143; 68; Conservative 0; Mismatches 0; Indels 0;
             34840: contig of 14325 bp in length 34840: contig of 14325 bp in length 54827: contig of 19987 bp in length gap of unknown length 74530: contig of 19703 bp in length 93245: contig of 18715 bp in length gap of unknown length 116394: contig of 21349 bp in length gap of unknown length 184655: contig of 68261 bp in length
                                                                                                                                                                                                                                                                                                                                                                                               /clone="RP11-144C15"
/clone_11b="RPC1-11 Human Male BAC"
35140 c 33570 g 51373 t 2 others
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Tilev, T., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McGurthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Maldrim, J., Mneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Naman, C.H., O'Connor, T., O'Connel, P., O'Nonl, D., Ollvar, T.M., Ollver, J., Peterson, K., Pierre, N., Pisant, C., Pollara, V., Raymond, C., Rilley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Tigillo, J., Vassillav, H., Vel, R., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Wiman, D., Ye, W.J., Young, G., Zuhon, A., and Zody, M., Milson, B., Wu, X., Wyman, D., Ye, W.J., M., Submission
                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This record contains 88 individual

* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
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f 785 bp in length
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10318: contig of 773 bp in
10418: gap of 100 bp
11205: contig of 787 bp in
6 11305: gap of 100 bp
12077: contig of 72 bp in
12077: gap of 100 bp
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12959: contig of 782 bp
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13855: contig of 796 bp
13955: gap of 100 bp
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08: gap of
5968: 7
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13356 14719; contig of 734 bp in length 14720 14720 contig of 778 bp in length 14720 1572; gen of 776 bp in length 15731 1572; gen of 776 bp in length 15739 1747; gen of 776 bp in length 15739; contig of 776 bp in length 15739; gen of 777 bp in length 15759; gen of 777 bp in length 15779; gen of 16770 bp in length 15779; g
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pineal gland 22966 GGATAATACCTITCAAGCIGCATGGCCCTCAGCAGATGAATCCATCACCAGCAGTATICC 22907 ggataatacctttcaagctgcatggccctcagcagatgaatccatcaccagcagtattcc 1489 2 (bases 1 to 4368)
Wang,X., Brownstein,M.J. and Young,W.S.
Direct Submission
Submitted (30-0CT-1996) LCMR, NIMH, 36 Convent Drive, MSC 4068, Bethesda, MD 20892-4068, USA Rattus norvegicus Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus 1 (bases 1 to 4368) 13-NOV-1996 ö Length 77043 Wang, X., Brownstein, M.J. and Young, W.S. 3rd. Sequence analysis of PG10.2, a gene expressed in the and the outer nuclear layer of the retina Brain Res. Mol. Brain Res. 41 (1-2), 269-278 (1996) 22 46421: gap of 100 bp 47201: contig of 780 bp in length 47201: contig of 780 bp in length 48095: contig of 794 bp in length 48095: contig of 794 bp in length 100 bp 4979: gap of 100 bp 100 Indels RNU76717 4368 bp mRNA ROD RALTUS norvegicus PG10.2 mRNA, complete cds. U76717 U76717.1 GI:1667596 3.0%; Score 125; DB 71; 100.0%; Pred. No. 1.9e-60; .ive 0; Mismatches 0; 3.0% Best Local Similarity 100.0 Matches 125; Conservative 46422 47202 48036 48196 48196 48980 49827 49827 50879 51650 51750 52523 52623 55102 55202 55980 56080 56874 56974 58635 58735 59546 59646 60414 50779 11111 22846 TCCTT 22842 1550 tcctt 1554 97038366 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ထ ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL 1430 RESULT RNU76717 LOCUS 셤 g 8 ò

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be preserved.
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EDLFNKNSLEYKALEQRFLELLVPYLQSNLSGGONLEILNFRNGSIVVNSRVKFAESV
PPNVNNAIYMLLEDFCTTAYQPWNLDIDKYSLOVESGDDANPCKFQACNEFSECLVN
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SOGHCEEFVSEFYIGITIASYVSLLLTVASAVYELTAKLLQAQNYRRERQRPTRROPD
SLSSYENAMKYNPATSRLAGCEQYBRPYSQHPFYSSASEEVIGGLSREEIRQMYESS
DLSKEEIQERWRILELYANDPEFAAFVREHEMEEL"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 65674)

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Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 38; Conservative 0; Mismatches 0;
                                                   l. .4368
/organism="Rattus norvegicus"
|O_xref="taxon:10116"
|90. .3909
                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAC52891.1"
/db_xref="G1:1667597"
ocation/Qualifiers
                                                                                                                                                                                                          'gene="PG10.2"
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21148: gap of 100 bp 121798: contig of 650 bp in length 109 22592: contig of 694 bp in length 100 bp 100 bp
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70 16357: contig of 688 bp in length 16457: gap of 100 bp 162 1744; contig of 687 bp in length 15 17244; gap of 100 bp 17919: contig of 675 bp in length 18 18790; gap of 100 bp 18790; 
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79: gap of 100 bp
20273: contig of 694 bp in length
373: gap of 100 bp
373: gap of 675 bp in length
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14102: gap of 100 bp
14782: contig of 680 bp in length
14882: gap of 100 bp
15569: contig of 687 bp in length
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38338: contig of
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40700: contig of
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39928: contig of
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52: contig of
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EURATYOLA; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 146547)

Saridqeman, A.

Direct Submitssion

L. Submitted (10-JUL-1998) E-mail enquires: humquery@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

On Jul 4, 1998 this sequence version replaced gi:3281979.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence is the entire insert of clone 511824. This sequence has been finished according to sequence map criteria as follows. An attempt is made
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HS511B24 146547 bp DNA PRI 23-NOV-1999 HOME Sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for I-Phosphatidylinositol 4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11) PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-Gamma-1 PLC-II, PLC-Gamma-1 Sinc Finger Homeobox protein and a 608 Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CPG island, ESTS, STSS and GSSS, complete sequence.
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3 49144; contig of 6
5 49244; gap of 10
5 49929; contig of 6
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48372: contig of
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43706: contig of
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47581: contig of
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/J0513 U07806 Z21625 L20632 M55632 AB000407 L07777; match:
ESTS AA855805 AA871201 AA623645 D55538 D54690 AA475125
T55685 F07589 R60159 AA868218 AA587119 AA653724 R76488
AA267891 R20925 AA814104 AA827288 C86359 AA189982 R32386
AA438250 AA215922 AA260815 AA203865 AA371144 AA830283
AA825116 AA28998 AA232866 AA792440 AA14395 AA345194
AA170792 AA792988 AA55255 AA146456 R91594 AA513865 R63040
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AA026178 AA987503 R69110 N83271 AA748864 R68389 T85685
AA333029 AA377110 AA556848 AA8511364 RA551396 R65749 R38217
R60159 AA809301 AA914511 AA769088 AA571578 R76622 AA933044
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join(<7958. 8101,9146. .9331,10547. .10615,11454. .11568,
13345. .13472,16872. .16966,17182. .17331,18371. .19663)
/gene="TOP1"
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13345. .13472,16872. .16966,17182. .17331,18371. .18473)
/gene="TOP1"</pre>
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to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. This sequence was generated from part of bacterial clone contigs human chromosome 20, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at http://www.sanger.ac.uk/RGP/Chr20
511B24 is from the library RCI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://worpac.med.buffalo.edu/ VECTOR: pCYPAC2.
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/note="LiME2 repeat: matches 627. .763 of consensus"
complement(6779. .6823)
/note="Alud repeat: matches 296. .250 of consensus"
complement(7748. .7892)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP3-511B24"
/clone_1lb="RPCI-3"
complement(672. .97)
/note="Aluxx repeat: matches 301. .1 of consensus"
complement(1348. .1462)
/note="Linepeat: matches 4845. .4733 of consensus"
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/note="Alusx repeat: matches 1. .298 of consensus"
complement(5387. .5988)
/note="match: GSS B52960"
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/product-"dJ511B24.1 (Topoisomerase I)"
/protein_id-"CAA18536.1"
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/product="dJ511B24.1 (Topoisomerase I)"
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/note="2 copies 39 mer 89% conserved"
complement(3104. .3165)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
/map="q11.2-12"
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TLQQQLKELTAPDENIPAKILSYNRANRAVAILCNHQRAPPKTFEKSMMLQTKIDAK
KEQLADARRDLKSAKADAKVMKDAKTKKVVESKKKAVQRLEEQLMKLEVQATDREENK
QIALGTSKLNYLDPRITVAMCKKWGVPIEKIYNKTQREKFAMAIDMADEDYEF"
/translation-"GEKDWQKYETARRLKKCVDKIRNQYREDWKSKEMKVRQRAVALY
FIDKLALRAGNEKEEGETADTVGCCSLRVEHINLHPELDGQEYVVEFDFLGKDSIRYY
                                                nkvpvekrvfknlolfmenkopeddlfdrlntgilnkhlodlmegltakvfrtynasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        // note="18" copies 2 mer tg 100% conserved" complement(22602. .22875) // note="AluSg repeat: matches 29%. .1 of consensus" 2296. .23047 // note="AluSg repeat: matches 137. .281 of consensus" 2296. .13047 // note="AluSg repeat: matches 137. .281 of consensus" complement(23273. .24163) // note="LiPAZ repeat: matches 891. .1 of consensus" complement(24014. .24379) // note="Lil repeat: matches 5390. .5025 of consensus" 24365. .24952 // note="Lil repeat: matches 4432. .5017 of consensus" complement(24953. .2521) // note="AluSa repeat: matches 29%. .1 of consensus" complement(25290. .25589) // note="AluSa repeat: matches 295. .2 of consensus" 25774. .26077 // note="LiMaz repeat: matches 586. .901 of consensus" 25774. .26077 // note="LiMaz repeat: matches 586. .901 of consensus" 25774. .26077 // note="LiMaz repeat: matches 586. .901 of consensus" 25124. .26418
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2553. .22588
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77555. .27847
77556. .28847 matches 1. .300 of consensus" 8720. .28847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20127. .20230
/note="match: GSS AQ016533"
complement(21628. .21830)
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19663
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/clone_lib-"Research Genetics/Cal Tech CITB-HSP-C (plates 195-384)"
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AL138917
AL138917.3 GI:7634251
HTG: HTGS_DRAFT.
runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 22; DB 41; Length 170891;
                                                                                                                                 13970: contig of 13970 bp in length gap of unknown length 3627: contig of 22657 bp in length gap of unknown length 64704: contig of 18077 bp in length gap of unknown length 64071: contig of 9367 bp in length gap of unknown length 72660: contig of 8589 bp in length 7360: contig of 4700 bp in length gap of unknown length 77360: contig of 4700 bp in length gap of unknown length
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44465 c 42708 g 40103 t
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/db_xref="taxon:9606"
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Matches 22; Conservative
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AL138917/c
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                                                                                                                55329
           /note="2 copies 24 mer 98% conserved"
31766. 33368
/note="putative CpG island"
/note="putative CpG island"
/note="putative CpG island"
5010(32700. 35734,55046. 55139,55282. 5532;57628. 57712,57818. 57901,58134. 58168,58379. 58451,58554. 58655,58891. 59009,59097. 59182. 59257. 59377,60109. 60277,60421. 60643,60626. 60727,60815. 61002,61370. 61570,61652. 61771,61855. 62035,63028. 63105,63343. 64465,67597. 67821,64633. 64702,65288. 65445,68828. 68989,6999. 69187,69303. 69487,69643. 70895)
                                                                                                                                                                                                                                                                                                                                                         /note-"match: cDNAs M34667 Y00301 X95346 J05155 M37238;
match: ESTS R76690 AA852993 AA441941 AA778666 AA587217
AA902444 AA641649 AA927359 AA447669 AA276604 AA442034
R76365 219499 N35819 AA927359 AA385590 AA906587 AA331680
W65062 AA215096 R24321 R57219 T28344 AA146590 F00147
AA018078 T07067"
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/product-*d4511824.2
(1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase
damma I (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1
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(bases 1 to 170891)

Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W.,
Fesman,K.H., Lander,E.S., McKernan,K., Munro,C., Richardson,P.,
Barna,N., Chang,A., Cooke,P., Daly,M.J., Forrest,C., Fripp,W.J.,
Gage,D., Geralgery,K., Hagos,B., Jacotot,L., Lane,M., MacKenzle,J.,
Marquis,N., McDermott,J., Moloney,N., Morrow,J., Nachman,A.,
Naylor,J., O'Connor,T., Peterson,K., Rollins,G., Spencer,J.,
Stilwell,J., Stone,C., Strickland,C., Sydney,K., Wilmer,F. and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 170891)
Hawkins, T.L., Birren, B.W., Fasman, K.H., Nussbaum, C. and Lander, E.S.
Genomic sequence from Human 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-MAY 1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Oct 2, 1997 this sequence version replaced 91:2257733. The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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*** SEQUENCING IN
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http://ftp.genome.washington.edu/RW/RepeatMasker.html.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contligs. The true order of the pleces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome 17 clone 303_E_14, PROGRESS ***, 20 unordered pieces.
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Pred. No. 1.9;
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AC002118.1 GI:2462727
HTG; HTGS_PHASE1.
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Best Local Similarity 100.
Matches 22; Conservative
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                                                            misc_feature
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DEFINITION
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REFERENCE
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RESULT 1 AC002118

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COMMENT

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Gaps

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Indels

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2197 others

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HS134E15 177163 bp DNA PRI 23-NOV-1999 Human DNA sequence from clone 134E15 on chromosome 6q21 Contains Blimp-1, apoptosis specific protein similar to yeast APG5 ESTs, GSSS and retroviral sequence, complete sequence.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177163)
Tubby, Direct Submission
Direct Submission
Submitted (19-AUG-1998) E-mail enquiries: humquery@sanger.ac.uk
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100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indels 0;
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fragment_chaln:3"

117903. .12466

/note="assembly_fragment:00532

fragment_chaln:3"

124767. .126003

/note="assembly_fragment:00300"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126104. 147223

/note="assembly_fragment:00304"

147324. 160327

/note="assembly_fragment:01083"

160428. 161556

/note="assembly_fragment:01083"
                                               14151. .47417

Incte assembly fragment:00210
fragment_chain:1"
47518. .51622
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fragment_chain:1"
51793. .65369
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fragment_chain:2"
/note assembly_fragment:01494
fragment_chain:2"
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fragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80047. .103635
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fragment_chain:2"
103736. .107122
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fragment_chain:2"
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fragment_chain:2"
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54119 a 31984 c 32447 g
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                       vector_side:left"
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HTG; Blimp-1.
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Best Local Similarity 100.0
Matches 22; Conservative
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Homo sapiens
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HS134E15/c
LOCUS
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently * consists of 16 contigs. The true order of the pieces is * not known and their order in this sequence record is * arbitrary. Where the contigs adjacent to the vector can be identified, they are labelled with 'clone_end' in the * feature table. Some order and orientation information * can tentatively be deduced from paired sequencing reads * which have been identified to span the gap between two * contigs. These are labelled as part of the same * 'fragment_chain', and the order and relative orientation * of the pieces within a fragment_chain is reflected in * this file. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as * soon as it is available and the accession number will be * preserved.

* 1450 contigs of 1450 bp in length; fragment_chain i * 51793 68343 contig of 1357 bp in length; fragment_chain i * 65470 68344 contig of 1357 bp in length; fragment_chain i * 65470 68345 contig of 1359 bp in length; fragment_chain i * 10732 contig of 1358 bp in length; fragment_chain i * 10733 117902 contig of 1358 bp in length; fragment_chain i * 10732 contig of 1358 bp in length; fragment_chain i * 10735 117002 contig of 1350 bp in length; fragment_chain i * 10732 117002 contig of 1300 bp in length

* 10736 12603 contig of 1327 bp in length

* 10737 12602 contig of 1328 bp in length

* 10732 17741 contig of 1300 bp in length

* 10502 17741 contig of 1300 bp in length

* 10502 17741 contig of 1300 bp in length

* 10503 contig of 1229 bp in length

* 10504 1525 contig of 1229 bp in length

* 10505 contig of 1229 bp in length

* 10507 contig of 1229 bp in length

* 10508 17741 contig of 1295 bp in length

* 10509 125003 contig of 1295 bp in length

* 105003 contig of 1295 bp in length

* 105003 contig of 1295 bp in length

* 105003 contig of 1295 bp 
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 171741)
                                                                                                   Parker.A.

Direct Submission
Submitted (20-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 21, 2000 this sequence version replaced gi:7024299.

Center: Sanger Center
Center: Sanger Center
Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: XGAP4, version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Bi4 Dye; 100% of reads
Consensus quality: 161469 bases at least Q40
Consensus quality: 165558 bases at least Q30
Consensus quality: 168131 bases at least Q20
Insert size: 170241; aum-of-contigs
Insert size: 160325; 10.6% error; agarose-fp
Quality coverage: 3.42x in Q20 bases; sum-of-contigs Quality
coverage: 3.63x in Q20 bases; agarose-fp

    14050
    note="assembly_fragment:00804
fragment_chain:1

                                                                                                                                                                                                                                                                                                                                                                                                Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- Summary Statistics
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: dJ354M18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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ORGANISM
                                                                                  REFERENCE
AUTHORS
                                                                                                                                             TITLE
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AA8058171 AA857721; match: AA743541 238498 T39272 AA921725
AA8058171 AA857721; match: AA76820"
AA807413; match: N94326 AA766820"
complement(15720. .16020)
(Anote="AluJo repeat: matches 302. .1 of consensus"
(Anote="MIR repeat: matches 48. .140 of consensus"
(Anote="MIR repeat: matches 299. .1 of consensus"
(Anote="AluSo repeat: matches 299. .1 of consensus"
(Anote="AluSo repeat: matches 299. .1 of consensus"
(Anote="AluSo repeat: matches 164. .36 of consensus")
(Anote="MIR repeat: matches 164. .36 of consensus")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Octop-lement(29028: .29070)

Anote-"NIR2 repeat: matches 145. .104 of consensus"
29179. .29383

Anote-"LimE3A repeat: matches 411. .613 of consensus"
Complement(30187. .30302)

Anote-"MIR repeat: matches 146. .20 of consensus"
30808. .31092

Anote-"Alusx repeat: matches 1. .298 of consensus"
32479. .3276

Anote-"Alusx repeat: matches 1. .298 of consensus"
32435. .33537

Anote-"Alusx repeat: matches 1. .291 of consensus"
3748. .34038

Anote-"Alusx repeat: matches 1. .291 of consensus"
Complement(35979. .36266)
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37441. .37512. .3944

Anote-"Alusx repeat: matches 302. .1 of consensus"
37441. .37512. .33744. .37512.
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/note="MER30 repeat: matches 2. .142 of consensus"
23412. .23704
/note="MER30 repeat: matches 1. .292 of consensus"
23705. .23801
/note="MER30 repeat: matches 133. .230 of consensus"
complement(424029. .24215)
/note="LIMB2 repeat: matches 915. .726 of consensus"
complement(25622. .25713)
/note="MIR repeat: matches 192. .97 of consensus"
26697. .26985
                                                                                                                                                                                                                                           /note="match: multiple ESTs; match: AA344205 AA372865 AA317110"
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/hote="match: multiple ESTs; match: AA730123 R25873"
prim_transcript 13946. .14238
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/note-"MER31 repeat: matches 254. 146 of consensus"
38965. 3240
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/hote="match: multiple ESTs; match: 242260 AA768582"
<14302. .14610
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/note="MER33 repeat: matches 158. .79 of consensus" 41730. 42041
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/note="MIR repeat: matches 47. .142 of consensus"
complement(29028. .29070)
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43357. .43473
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                                                                                                                                                                                   prim_transcript <14302. .14610
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                                                                                                                                                                                                                                                                                                                           <14664. .>15126
prim_transcript <12902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
134E15 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.

Location/Qualifiers

/ Chromosome="Homo sapiens"
/ Chromosome="6"
                                                                                   Where differences are found these are annotated as variations variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence is the entire insert of clone 134E15. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFRRGSPEMPFYPRVYPPIRAPLPEDFLKASLAYGIERPTYITRSPIPSSTTPSPSA
RSSPOGSIKSSSPHSSPGWTVSPYGSGEHRDSYALLANSTGFEGLGSFEGAPLPH
IPPALIPSTANAYPPIRAPLPPGGNUNGLSAYLLANSTGFEGLGSFEGAPLPH
IPPALIPSTLPSSTRASPRALLOPPGHREAVSHMGINFGLFPRLCPVYSNLLGGGS
LPHPMLMPTSLPSSLPSDGARRLLOPPHPRETVTVPAPHSAFSFTGAAAASMKOKACSPF
SGSPTAGTAATABHVVORKATSAAMAAPSSDEAMNLIKNKNWTGYKTLFPPLKKONG
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PENDPLENYPWKNKQETAVVRKEREFTGLKVSLORNMGNGLLSSGCSLFESSDLPLMKLP
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TQSSLKQPSTEKNELCPKNVPKREYSVKEILKLDSNPSKGKDLYRSNISPLTSEKDLD
   Clone requests: clonerequest@sanger.ac.uk
On Aug 5, 1998 this sequence version replaced gi:3355451.
During sequence assembly data is compared from overlapping clones.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jóin(<802. 921,3766. 3867,4487. 4739,10012. 11120,
11558. 11686,12098. 12673)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .94
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/gene-"dJ134E15.1"
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repeat_region repeat_region

misc_feature

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NOTE: This is a 'working draft' sequence. It currently consists of 48 conigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                       Center: Washington University Genome Sequencing Center
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/note="THELB repeat: matches 1. .364 of consensus"
57245. .57330
/note="THELB-INTERNAL repeat: matches 1. .86 of consensus"
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On Mar 10, 2000 this sequence version replaced gi:7105562.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          Acce—"Alusg repeat: matches 299. .1 of consensus 46124. .46410 complement(46516. .46698)

Anote—"NIK repeat: matches 185. .3 of consensus" A733. .4750

A733. .4750

A7336. .48548

A3356. .48548

A3356. .48548

A00te—"MIK repeat: matches 13. .258 of consensus" A1356. .48548

Anote—"MIK repeat: matches 30. .3 of consensus" Complement(45685. .49976)

Anote—"MIK repeat: matches 55. .151 of consensus" A1046—"MIK repeat: matches 55. .151 of consensus" A1046—"MIK repeat: matches 56. .207 of consensus" A1046—"MIK repeat: matches 56. .207 of consensus" A1046—"MIK repeat: matches 15. .133 of consensus" A1046—"MIK repeat: matches 15. .133 of consensus" A1046—"MIK repeat: matches 15. .133 of consensus" A1046—"MIK repeat: matches 153. .46 of consensus" A1046—"MIK repeat: matches 10. .133 of consensus" A1046—"MIK repeat: matches 30. .1 of consensus" A1046—"MIK repeat: matches 30. .280 of consensus" A1046—"MIK repeat: matches 30. .280 of consensus" A1046—"MIKE repeat: matches 30. .380 of consensus" A1046—"MIKE A10486 repeat: matches 30. .380 of consensus" A1046—"MIKE A10486 repeat: matches 30. .380 of consensus" A1046—"MIKE A10486 repeat: matches 847. .483 of consensus" A1046—"MIKE A10486 repeat: matches 847. .483 of consensus"
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/note="THEIB-INTERNAL repeat: matches 1212. .1580 of
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/note="THELB repeat: matches 1. .352 of consensus"
complement(58034. .5825)
/note="LiMBG repeat: matches 510. .320 of consensus"
complement(58793. .59097)
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'note-"AluSg repeat: matches 299. .1 of consensus'
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Pred. No. 1.9;
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HTG; HTGS_PHASE1.
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Waterston, R.H.
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Waterston, R.H.
Direct Submission
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VERSION KEYWORDS SOURCE ORGANISM

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REFERENCE AUTHORS

TITLE JOURNAL REFERENCE AUTHORS

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COMMENT

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UMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, sequents. Contig_ID: 00507 Length: 2401bp Contig_ID: 00507 Length: 2401bp Contig_ID: 00557 Length: 2384bp Contig_ID: 00556 Length: 1250bp Contig_ID: 00556 Length: 1250bp Contig_ID: 00556 Length: 1375bp Contig_ID: 00565 Length: 1675bp Contig_ID: 00565 Length: 1675bp Contig_ID: 00565 Length: 1875bp Contig_ID: 00565 Length: 1875bp Contig_ID: 01072 Length: 2465bp Contig_ID: 01072 Length: 1875bp Contig_ID: 0154 Length: 1135bp Contig_ID: 0154 Length: 1135bp Contig_ID: 01554 Length: 1135bp Contig_ID: 01566 Length: 1148bp Contig_ID: 01566 Length: 1154bp Contig_ID: 02405 Length: 1154bp Contig_ID: 02405 Length: 1154bp Contig_ID: 02406 Length: 02406 Length: 02406 Length:
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Contig_ID: 00965 Length: 1073bp
Contig_ID: 000967 Length: 1485bp
Contig_ID: 01072 Length: 2169bp
Contig_ID: 01208 Length: 2695bp
Contig_ID: 01208 Length: 2695bp
Contig_ID: 01384 Length: 135bp
Contig_ID: 01544 Length: 135bp
Contig_ID: 01938 Length: 1135bp
Contig_ID: 02465 Length: 1154bp
Contig_ID: 02466 Length: 1154bp
Contig_ID: 02760 Length: 1154bp
Contig_ID: 03704 Length: 1569bp
Contig_ID: 03704 Length: 1000bp
Contig_ID: 03738 Length: 1000bp
Contig_ID: 03739 Length: 1000bp
Contig_ID: 03739 Length: 1000bp

* NOTE: This Ta "working draft' sequence record is
* arbitrary Caps between the contigs are represented as
* Is not known and their order in this sequence record is
* arbitrary Caps between the contigs are represented as
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
On Feb 16, 2000 this sequence version replaced gi:6967355.
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4036: gap of ...
35171: contig of 1135 bp ...
35971: contig of 3041 bp in length ...
39012: contig of 3041 bp in length ...
ap of ...
600 bp ...
700 f 1001 bp in length ...
701 f 1001 bp in length ...
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42767: contig of 1154 bp in length
567: gap of 800 bp
47713: contig of 4146 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1865: gap of 800 bp 4266: contig of 2401 bp in length 5066: gap of 800 bp 7450: contig of 2384 bp in length 8250: gap of 800 bp 9500: contig of 1250 bp in length
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202146: contig of 2142 bp in length
2946: gap of 800 bp
30346: contig of 1000 bp in length
4746: gap of 800 bp
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1066 1865: gap of 800
1866 4266: contig of 24
4267 5066: gap of 800
5067 7450: contig of 23
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Submitted (10-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Homo sapiens chromosome 6 clone RP3-474G24, *** SEQUENCING IN PROGRESS ***, 20 unordered pleces.
AL133509 AL133509.6 GI:6983041
HTG; HTGS_PHASE1; HTGS_DRAFT.
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/db_xref="taxon:9606"
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JOURNAL
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* 204747 205746: contig of 1000 bp in length.

FEATURES

Location/Qualifiers

1. .205746

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/Chromosome="6"
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Search completed: September 3, 2000, 17:19:46 Job time: 24903 sec

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9b_htg21:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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/db_xref="61:6118566"

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TESTERMYRMSTHRETDLARHENFRRAFFPGVRVCPQESWKQILDSLQAYYRLRVC
ORAVREAYRFELDRIPDTGEYODWYSICOGFFFCLEDIGKNESNSGEHLDLLQQRIKG
RSFPDRKDEISAEKTLGEPGETIVISTDVANVSLGBPPLTPDDTLLNEILDNTLNDTK
MPTTREETERAVLEGORVELGSTVNVGFKABLADGOSPYVGLAGKSQLQMOKIFK
LPGFKKIHVLGFRRKKEKDGSSSTEMQLTAIFKRHSAEARSPASDLLSFDSNKIESEE
VRGTWERDROPEILTPRADKRLISRALEBGSLDVGTTGTDEIAGSLPARGPDTG
SELPYSFAVITEDATLSFELPPVEPQLETVGCAEHGLPDTGWSPPRAASTSLSEAPFF
FMASSIFSLTDQGTTDTMATDQTMLVPGLTIPFSDYSAISOLAGISHPRASSDDSRS
                                                                                                                                          SAGGEDMVRHLDEMDLSDTPAPSEVPELSEYVSVPDHFLEDTTPVSALQYITTSSMTI
APKGRELVVFFSLRVANMAFSNDLFNKSSLEYRALEQOFTQLLVPYLRSNLTGFKQLE
DQADPROSTVYNSKNKFRSYPYNLTKAVHGYLEDFRRAAAQQLHLETDSYSLNIEPA
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QGKGAPCRLPDHSENGKFRONQNNKVISKRNSELLTVEYEEFNHQDWEGN"
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AC022671 Homo sapi
AL035477 Plasmodiu
AC024825 Homo sapi
U87514 Dictyostell
AL17200 Caenorhab
AL35283 Homo sapi
AC01349 Homo sapi
AC04116 Mus muscu
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AC021254 Homo sapi
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Kuehn, M.H. and Hageman, G.S.

Direct Submission
Submitted (10-FEB-1998) Ophthalmology and Visual Sciences,
University of Iowa, 200 Hawkins Drive, 11190E PFP, Iowa City,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 3268)
Kuehn, M.H. and Hageman, G.S.
Direct Submission
Submitted (26-OCT-1999) Ophthalmology and Visual Sciences,
University of lowa, 200 Hawkins Drive, 11190E PFP, Iowa City,
52240, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"interphotoreceptor matrix proteoglycan 150"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3268)
Kuehn, M.H. and Hageman, G.S.
Expression and characterization of the IPM 150 gene (IMPG1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product, a novel human photoreceptor cell-associated chondroitin-sulfate proteoglycan Matrix Biol. 18 (5), 509-518 (1999)
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On Oct 26, 1999 this sequence version replaced g1:2906231
Location/Qualifiers
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/db_xref="taxon:9606"
/cbromosome="6"
/cbromosome="6"
/cbromosome="6"
/tissue_type="retina"
1. 3268
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SVU90554
SYNCLOSHP
PIP404CG
                                                    PFMAL4P4
AC024285
CEY50287514
CEY50287C1
CROSFC1
AC013349
PFMAL3P7
AC04186
AC046180
AC031982
AC031254
CLOCLES
SYU90555
              AC022851
AC021008
AC022671
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/codon_start=1
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/gene="IMPG1"
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AF047492.2 GI:6118565
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TATGACCATTGCCCCCAAGGGCCGAGAGCTGGTAGTGTTCTT acaattcacacagctgctggttccatatctacgatccaatct tgcagcccaacactccatctggaatagacagctactctt aaagttccaaaatcaacaaaataacaaggtaatcagtaaaag **AAAGTTCCAAAATCAACAAATAACAAGGTAATCAGTAAAAG** 

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Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1235)

Felbor, U., Gehrig, A., Sauer, C.G., Marquardt, A., Kohler, M., Schmid, M. and Weber, B.H.

Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate for Gq-linked retinopathies

Gytogenet. Cell Genet. 81 (1), 12-17 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSIMPG17 1235 bp DNA PRI 28-OCT-1998 And sapiens interphotoreceptor matrix gene (IPM150), exon 17 and complete cds.
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2994 gtagtgagtgtatatatgctccacactacgtctgataaacacaaacctcagtattcagtt
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join AF017760.1:<1. .223, AF017761.1:97. .330,
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AF017764.1:107. .171, AF017765.1:139. .242,
AF017766.1:163. .303, AF017769.1:95. .339,
AF017770.1:148. .224, AF017773.1:271. .349,
AF017772.1:144. .676, AF01773.1:111. .330,
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/db_xref="taxon:9606"
/chromosome="6"
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/gene="IPM150"
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Pred. No. 2.7e-174;
0; Mismatches 15; Indels 1
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/gene="IPM150"
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AL157379.2 GI:7159486
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1 (bases I to 816)

Schor, U., Gehrig, A., Sauer, C.G., Marquardt, A., Kohler, M., Schmid, M. and Weber, B.H.
Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate for 6q-linked retinopathies
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Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. and Weber, B.H.F.
Assessment of a novel interphotoreceptor matrix gene (IPMISO)
localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI)
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                         746 TGATAGTCAAAATGATCATAAGCCAGGTTTGCTTCCACCTTCCCTGAAAATTTTACTCAC 805
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                                                                                                                                                                                 Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F. Direct Submission
Submitted (09-AUG-1997) Humangenetik, Universitaet
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Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="6"
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Submitted (22-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire, Submitted (22-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 6, 2000 this sequence version replaced gi:7009540.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 194704)
Sims, A.
Direct Submission
Submitted (22-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire,
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                                                                                      DB 11; Length 816;
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16.4%; Score 535.8; DB 11
Best Local Similarity 99.6%; Pred. No. 3.4e-111;
Matches 537; Conservative 0; Mismatches 2;
255
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Contig_ID: 00934 Length: 10010bp
Contig_ID: 00934 Length: 10010bp
Contig_ID: 01026 Length: 2716bp
Contig_ID: 01121 Length: 2283bp
Contig_ID: 01185 Length: 10059bp
Contig_ID: 01185 Length: 1779bp
Contig_ID: 01370 Length: 1779bp
Contig_ID: 01386 Length: 1488bp.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 28 contigs. The true order of the pleces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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82931: contig of 1028 bp in length
83731: gap of 800 bp
91019: contig of 7288 bp in length
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Length: 1873bp
Length: 1873bp
Length: 1124bp
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Length: 286bp
Length: 15535bp
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98660: cont
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Eukaryotza, Metazoa; Chordata; Cranlata; Vertebrata; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 444)
Schmid, M. and Weber, B.H.
Schmid, M. and Weber, B.H.
Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate for 6q-linked retinopathies
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 444)
Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E.
and Weber, B.H.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany Location/Qualifiers
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Homo sapiens interphotoreceptor matrix gene (IPM150), exon 10.
AF017769
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                                                                  Query Match 7.6%; Score 249; DB 11; Length 444; Best Local Similarity 100.0%; Pred. No. 3.9e-46; Matches 249; Conservative 0; Mismatches 0; Indels
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Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
Direct Submission
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/db_xref="taxon:9606"
/chromosome="6"
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                                                                                                                                                    Homo sapiens
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/protein.id="AAC03788.1"
/db_xref="d1:2906230"
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RTGERSETIVVSTDVASVSLGPFPYTPDDTLLNEILDNALNDTKMPTTERETELAVS
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                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
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                                                                                                                                                                                   Kuehn, M.H. and Hageman, G.S.
Characterization And Complete CDNA Sequence Of IPM 150, A Novel
Human Photoreceptor Cell-Associated Chondroitin-Sulfate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 tttttcccaacgggggttaaagttgtccacaggaatccatgaaacagattttagacagt 403
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                                                                                                                                                                                                                                                       2 (bases 1 to 555)
Kuehn, M. H. and Hageman, G.S.
Direct Submission
Submitted (10-FEB-1998) Ophthalmology and Visual Sciences,
University of Iowa, 200 Hawkins Drive, 11190E PFP, Iowa City,
52240, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 CTTCAAGCTTATTATAGATTGAGAGTGTGTCAGGAAGCAGTATGGGAAGCATATCGGATC 123
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Pred. No. 1.5e-105;
0; Mismatches 25;

    .555
    /organism="Macaca fascicularis"
/db_xref="taxon:9541"

                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="retina"
<1. .>555
/note="IPM 150"
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                   AF047491.1 GI:2906229
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Best Local Similarity 95.5%;
Matches 526; Conservative
                                                                                   crab-eating macaque.
Macaca fascicularis
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                 mRNA, partial cds. AF047491
                                                                                                                                                                                                                                    Proteoglycan
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Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. and Weber, B.H.F.
Assessment of a novel interphotoreceptor matrix gene (IPMI50)
localized to 6q14.2-q15 in autosomal dominant stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI)
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1 (bases 1 to Sases 1 to Sases 1 to Sases 1 to Sases 2 to Sases 2 to Sases 2 to Sases 3 to Sases 2 to Schmid, M. and Weber, B.H. Schmid, M. and Weber, B.H. Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate for Gq-linked retinopathies
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am
 1194 aaaggetgateageaaageaetagaggaagaacaatetttggatgtggggacaatteagt 1253
                   190 taaaagatateteceattaacatataeceattetgaaaetaaagaeatagaeaateeeceeag 249
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Homo sapiens interphotoreceptor matrix gene (IPM150), exon 2.
AF017761.1 GI:3800716
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Felbor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.
Direct Submission
Submitted (09-AUG-1997) Humangenatik mainter
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99.6%; Pred. No. 1.7e-43;
11ve 0; Mismatches 1
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Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="6"
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requests: One beginning in the control of sequence version replaced gi:7009540.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may phage etc. Order of segments is not known; 800 n's separate segments. Contig_LD: 00025 Length: 6617bp

Contig_LD: 00151 Length: 1873bp
                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 194704)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (22-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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Contig_ID: 01026 Length: 2716bp
Contig_ID: 01026 Length: 2716bp
Contig_ID: 01121 Length: 2031bp
Contig_ID: 01186 Length: 10059bp
Contig_ID: 01186 Length: 1779bp
Contig_ID: 01370 Length: 1779bp
Contig_ID: 01386 Length: 1498bp.
* NOTE: This is a "working draft' sequence. It currently
consists of 28 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                    Homo sapiens chromosome 6 clone RP1-62L18, *** SEQUENCING IN PROGRESS ***, 28 unordered pieces.
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HTG; HTGS_PHASE1; HTGS_DRAFT
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Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate for 6q-11nked retinopathies
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
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1 (bases 1 to 448)

Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.

Direct Submission
Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am
  1930 ggagcaacaattcacacagctgctggttccatatctacgatccaatcttacaggatttaa 1989
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 448)
Felbor, U., Gehrig,A., Sauer,C.G., Marquardt,A., Kohler,M.,
Schmid,M. and Weber,B.H.
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Location/Qualifiers
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/organism="Homo sapiens"
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/chromosome="6"
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Pred. No. 1.7e-43;
0; Mismatches 1; Indels 0; G
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f 15535 bp in length
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03: contig of 19995 bp in length
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f 1028 bp in length
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f 5047 bp in length
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40287: contig of 1165 bp in length
41087: gap of 800 bp
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f 7288 bp in length
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100575: contig of 1115 bp in length
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7 194704: contig of 1498 bp in length.
Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="6"
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38322: contig of
28910: gap of 8
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2863 AAATCCTCAACTTCAGAAATGGCAGCATTGTGGGGAACAGTCGAATGAAGTTTGCCAATT

ctgtgccgtataacctcaccaaggctgtgcacggggtcttggaggattttcgttctgctg 

1938 aattcacacagctgctggttccatatctacgatccaatcttacaggatttaagcaacttg 1997 

1878 tggccttctccaacgacctgttcaacaagagctctctggagtaccgagctctggagcaac 1937

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cagcccaacaattcatctggaaatagacagctactctcaacattgaaccagctgatc 2177 2983 CCTACAATACCATGAACTTGGCTATTGATAAATACTCTTTGATGTGGAATCAGGTGATG 3042

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3103 GGAGTGGAGAAGCAAAGTGCAGGATGCTTCCCTGGATACCTGAGTGTGGAAGAAGAAGAACGCCCT 3162

RESULT 11 AF173155 LOCUS

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SSELSREEIQERMRVLELYANDPEFAAFVREQQVEEV"
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Marmalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

( 1) (Bases 1 to 3989)
Acharya,S., Foletta,V.C., Lee,J.W., Rayborn,M.E., Rodriguez,I.R., Young,W.S. 3rd and Hollyfield,J.G.
SPACRCAN, a novel human interphotoreceptor matrix
hyaluronan-binding proteoglycan synthesized by photoreceptors and
                                                                              06-MAR-2000
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Foletta, V.C. and Young, W.S.
Direct Submission
Submitted (09-JUN-1999) SNGE, NIMH, 36 Convent Dr, MSC 4068, Bethesda, MD 20892-4068, USA
                                                                      AF157624 3989 bp mRNA PI
Homo sapiens Spacrcan mRNA, complete cds.
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Enkaryota; Marazoa; Chordata; Craniata; Vertebrata; Mammalia; Enkaryota; Matazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

Entheria: Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 4165)

MOlecular characterization and genomic mapping of human IPM 200, a second member of a novel family of proteoglycans

LM MOL Cell Biol. Res. Commun. 2, 103-110 (1999)

E 2 (bases 1 to 4165)

S Xuchn, M. H. and Hageman, G.S.

Direct Submission

AL Submitted (28-JUL-1999) Ophthalmology, University of Iowa, 2501

Crosspark Rd,, Coralville, IA 52241, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mimfPlFGKISLGILIFVLIEGDFPSLTAQTYLSIEEIQEPKSA
VSFLLPEESTDLSLATKKKQPLDRRETERQWLIRRRRSILFPNGVKICPDESVAEAVA
Homo sapiens interphotoreceptor matrix proteoglycan 200 (IMPG2) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"interphotoreceptor matrix proteoglycan 200"
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6.2%; Score 203.4; DB 50; Length 3989; 63.7%; Pred. No. 8.6e-36; Live 0; Mismatches 176; Indels 0;

Best Local Similarity 63.7 Matches 309; Conservative

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Query Match

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Pred. No. 8.6e-36;
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Best Local Similarity 63.7%;
Matches 309; Conservative
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U76717.1 GI:1667596

Norway rat

VERSION KEYWORDS SOURCE

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/db_xref="G1:1667597"
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BIEBWTPGPOFPPAARDIAESBIQLACKQYSEELFDPSSALYKILVEBETSEVEKAFT
GLPGTKGIHVLDFRESPENGAGSTDVHYAVFRGEALSWITTWDLISLHSWKVERHGLVE
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STTLONTYSTLASSPSYLGGSSLTLHKYPPAULQIDLYVAPEGHTSGSS
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                                                                                                                                               Wang, X., Brownstein, M.J. and Young, W.S. 3rd.
Sequence analysis of PG10.2, a gene expressed in the pineal gland and the outer nuclear layer of the retina
Brain Res. Mol. Brain Res. 41 (1-2), 269-278 (1996)
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Wang,X., Brownstein,M.J. and Young,W.S.
Direct Submission
Submitted (30-ocr-1996) LCMR, NIMH, 36 Convent Drive, MSC 4068,
Bethesda, MD 20992-4068, USA
Location/Qualifiers
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                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 4368)
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    Rattus norvegicus
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2 (bases 1 to 310)
Gehrig,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.E. and Weber,B.H.F.
and Weber,B.H.F.
and Weber,B.H.F.
localized to 6914.2-915 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (bases 1 to 310)
Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
Direct Submission
Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany
Location/Qualifiers
  2271 gatatgacagccaggggagcctggacggtctggaaccaggcctctgtgg-cctggcacaa 2329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 GATATGACAGCCAGGGGAGCCTGGACGGTCTGGAACCAGGCCTCTGTGGCCCTGGCACAA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 agttcaaggaactaaagatatctccattaacatataccattctgaaactaaagacataga 237
                                                                                                                                                                                                                            Homo sapiens interphotoreceptor matrix gene (IPM150), exon 1. AF017760 GI:3800715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                     Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 310)
Felbor,U., Gehrig,A., Sauer,C.G., Marquardt,A., Kohler,M., Schmid,M. and Weber,B.H.
Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 174.4; DB 11; Length
Pred. No. 3.3e-29;
0; Mismatches 37; Indels
                                                                          for 6q-linked retinopathies
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
98358139
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/db_xref="taxon:9606"
/chromosome="6"
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<1. .156
/gene-"IPM150"
47 c
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<1. .156
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Best Local Similarity 84.6%;
Matches 219; Conservative
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Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. and Weber, B.H.F. and Weber, B.H.F. and Weber, B.H.F. of a novel interphotoreceptor matrix gene (IPM150) localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDR1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHMIAL, AND WEDET, B.H.

SCHOMIC ORGANIZATION and chromosomal localization of the
interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate
for 6q-linked retinopathies
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
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110 CTAATGTCAACAACGCCATATATATGATTCTGGAAGACTTTTGTACCACCGCCTACCAAA 3169
                                                                                                                                                                          3230 CTTGCAAGTTTCAGGCCTGTAATGAATTTTCTGAATGTTTGGTAAATCCATGGAGTGGAG 3289
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Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
Direct Submission
Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Hubland, Wuerzburg D-97074, Germany
                                                                                                                                                                                                                                                                                                                                HSIMPG15 477 bp DNA PRI 28-OCT-1998
Homo sapiens interphotoreceptor matrix gene (IPM150), exon 15.
AF017774
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Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 477)
Pelbor, U., Gehrid, A., Sauer, C.G., Marquardt, A., Kohler, M.,
Schmid, M. and Weber, B.H.
                                                                            2151 acteteteaacattgaaccagetgateaagcagatecetgeaagtteetggeetgegg
                                                          aactccatctggaaatagacagctactctcaacattgaaccagctgatcaagcagatc
                                                                                                                                                                                                              2247 aagoggagtgtogotgoaaacoaggatatgacagocaggggagootggacggto 2300
                                                                                                                                                                                                                                    3290 AAGCAAAGTGCAAATGCCACCCTGGGTACCTGAGTGGAATGAACTGCCTTGTC 3343
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    477
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="6"

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71. .269
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Best Local Similarity 93.7%
Matches 208; Conservative
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Length 310;

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By Washers 1 to 422)

Sehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. and Weber, B.H.F.

Assessment of a novel interphotoreceptor matrix gene (IPMI50) localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI) upublished

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S (Dasses 1 to 422)

RS Felbor, U., Kuchn, M., Hageman, G.S. and Weber, B.H.F.

Direct Submission

Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany

Location (16-AUG-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSIMPG03 422 bp DNA PRI 28-OCT-1998
Homo sapiens interphotoreceptor matrix gene (IPM150), exon 3.
AF017762.1 GI:3800717
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 422)
Felbor, U., Gehrig, A., Sauer, C.G., Marquardt, A., Kohler, M.,
Schmid, M. and Weber, B.H.
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    .422
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="6"

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112. .278
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                                                        238 caatcccccaagaaatgaa 256
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